

Copyright (C) 1993 - 2005 Compugen Ltd.	Gendcore version 5.1.6	Q66gt4 ratus norvegicus	Q66gt4 ratus norvegicus
Run on:	June 1, 2005, 09:34:17 ; Search time 114 Seconds (without alignments)	Q6d739 erwinia carotovora	Q6d739 erwinia carotovora
Title:	US-10-617-876-1	Q9axh1 phiscomitreus	Q9axh1 phiscomitreus
Perfect score:	668	Q87sy8 listeria monocytogenes	Q87sy8 listeria monocytogenes
Sequence:	1 MANKMQPTISTANKIVWSD.....NAGIGFLDPTAAIVSDDTTA 131	Q85571 methanococcus	Q85571 methanococcus
Scoring table:	BLOSUM62	Q8fb3 escherichia coli	Q8fb3 escherichia coli
Searched:	Gapop 10.0 , Gapext 0.5	Q84147 xenopus laevis	Q84147 xenopus laevis
Total number of hits satisfying chosen parameters:	1612378	Q8avm9 xenopus laevis	Q8avm9 xenopus laevis
Minimum DB seq length: 0		Q9n9g7 phallusia major	Q9n9g7 phallusia major
Maximum DB seq length: 2000000000		Q6bgk7 paramyces	Q6bgk7 paramyces
Post-processing: Minimum Match 0% Maximum Match 100%		Q7wrf3 streptomyces	Q7wrf3 streptomyces
Database :	UniProt 03; * 1: uniprot_sprot: 2: uniprot_trembl: Gapop 10.0 , Gapext 0.5	Q9ai69 helicobacter pylori	Q9ai69 helicobacter pylori
Searched:	1612378 seqs, 512079187 residues	Q8ib85 orya sativa	Q8ib85 orya sativa
Total number of hits satisfying chosen parameters:	1612378	Q14679 homo sapiens	Q14679 homo sapiens
Post-processing: Minimum Match 0% Maximum Match 100%			
Post-processing: Listing first 45 summaries			
Post-processing: Query Match 0% Best Local Similarity 100.0%; Score 668; DB 2; Length 131; Matches 131; Conservative 100.0%; Pred. No. 8.1e-60;			
Post-processing: Summary 1			
Post-processing: Summary 2			
Post-processing: Summary 3			
Post-processing: Summary 4			
Post-processing: Summary 5			
Post-processing: Summary 6			
Post-processing: Summary 7			
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Post-processing: Summary 347		</td	

Putative lipoprotein lppK precursor.
 Name=lpk;
 OrderedIhcocuNames=ML1315;
 ORNames=MCB2533_11C, B2126_P3_115;
 Mycobacterium leprae.
 OC
 Bacteria; Actinobacteria; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1769;
 [1]
 SEQUENCE FROM N.A.
 Smith D.R., Robison K./ Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 STRAIN=TN; PubMed=21128732; DOI=10.1038/315059006;
 Cole S.T., Eglimeier K., Parkhill J., James K.D., Thomson N.R.,
 Wheeler P.R., Honre N., Garnier T., Churcher C.M., Harris D.E.,
 Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 Murphy I.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL 409:1007-1011 (2001).
 [-] SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (POTENTIAL). Belongs to the MTB12 family.
 CC -|- SIMILARITY: Belongs to the MTB12 family.

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DR U00017; AAA7217_1;
 EMBL; AL035310; CAA2925_1; -;
 PIRBL; S72877; S72877;
 Leproma ML1315; -;
 PROSITE PS00013; PROKR_LIPOPROT_S;
 Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
 Palmitate; Signal. Potential.
 SIGNAL 1 26 Putative lipoprotein lppK.
 FT CHAIN 27 194 S-diacylglycerol cysteine (By similarity).
 FT LIPID 27 27 N-palmitoyl cysteine (By similarity).
 SQ SEQUENCE 194 AA; 20460 MW; E975262FC3218A6 CRC64;

Query Match 12.0%; Score 80; DB 1; Length 194.
 Best Local Similarity 25.0%; Pred. No. 6.4%;
 Matches 30; Conservative 10; Mismatches 54; Gaps 6;
 Qy 8 PITSTKTVWS--DPTRETTFSASILLRORVKYIAANVSCQYVSYTK----RPAP 60
 Db 110 PMTFPTANNIAWSNKNPSDVLATIS-----VNIAQTN-----SVPSPFMEFTPP 154
 Qy 61 KPEGCCADAVCIMPNENOSIRTIVSGSAENLATLKAETWTHKRYNDTLFASGNAGLGFLDP 120
 Db 155 PPQ-----QSWSQLSKRTADMLLFGNNS-GLTNP 182

RESULT 3
 IL6B HUMAN STANDARD; PRT; 918 AA.
 ID IL6B_HUMAN STANDARD;
 AC P40189; Q9UQ41;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
 DE 6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M
 DE receptor) (CD130) (CD130 antigen).
 DE Name=IL6ST;
 GN OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 OX RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Myeloma, and Placenta;
 RX MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;
 RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Hashimoto T.,
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RT sp130.;"
 RN RL Cell 63:1149-1157 (1990).
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=synovium;
 RX MEDLINE=31041529; PubMed=10880057;
 RA Tanaka M., Kishimura M., Okaki S., Osakada F., Hashimoto H., Okubo M.,
 RA Murakami M., Nakao K.;
 RT "Cloning of novel soluble gp130 and detection of its neutralizing
 RT autoreactive antibodies in rheumatoid arthritis.";
 RT J. Clin. Invest. 106:137-144 (2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE LINKAGE SITES.
 RX MEDLINE=21263388; PubMed=11098061; DOI=10.1074/jbc.M009979200;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "Determination of the disulfide structure and N-glycosylation sites of
 RT the extracellular domain of the human signal transducer gp130.";
 RL J. Biol. Chem. 276:8244-8253 (2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE=98169383; PubMed=9501088; DOI=10.1093/emboj/17.6.1665;
 RA Bravo J., Stanton D., Heath J.K., Jones B.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674 (1998).
 CC -|- FUNCTION: Signal-transducing molecule. The receptor systems for
 CC IL6, LIF, OSM, CNTR, CT1 can utilize gp130 for initiating
 CC signal transmission. Binds to IL6/IL6R (alpha chain) complex,
 CC resulting in the formation of high-affinity IL6 binding siteS, and
 CC transduces the signal. Does not bind IL6. May have a role in
 CC embryonic development (By similarity).
 CC -|- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC -|- SECRETED (isoform 2).
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoID=p40189-1; Sequence=Displayed;
 CC Name=2; Synonyms=GP130-RAPS;
 CC IsoID=p40189-2; Sequence=VPSP_001684; VSP 001685;
 CC -|- TISSUE SPECIFICITY: Found in all the tissues and cell lines
 CC examined. Expression not restricted to IL-6 responsive cells.
 CC -|- DOMAIN: The WSXWS motif appears to be necessary for proper Protein
 CC folding and thereby efficient intracellular transport and cell-
 CC -|- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -|- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
 CC (RA) but it is not specific to patients with RA.
 CC -|- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 2.
 CC -|- SIMILARITY: Contains 5 fibronectin type III domains.
 CC -|- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -|- SIMILARITY: Contains 1 CD guide CP130 entry;
 CC -|- DATABASE: NAME=PROK; NONE=CD guide CP130 entry;
 CC WWW=<http://www.ncbi.nlm.nih.gov/prokcd/cd130.htm>.
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EMBL; M57210; AAA59155.1; -.
EMBL; AB015706; BAA78112.1; -.
PIR; A36337; A36337.
PDB; 1B78; NMR; @=21'-325'.
PDB; 1BQU; X-ray; A/B=119-333.
PDB; 1I1R; X-ray; A=23-325.
Genew; HGNC:6021; IL6ST.
MIM; 600694; -.
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0004915; F: interleukin-6 receptor activity; TAS.
GO; GO:0004924; F: oncostatin-M receptor activity; TAS.
GO; GO:0004872; F: receptor activity; TAS.
GO; GO:0007166; P: cell surface receptor linked signal transdu.
GO; GO:0006955; P: immune response; TAS.
InterPro; IPR002996; Cytkn_recept_B/G.
InterPro; IPR0031961; FN_1IT.
InterPro; IPR008557; _N_III-like.
InterPro; IPR003529; Hemprecept_1302.
InterPro; IPR010457; Lep_receptor_Ig.
PFam; PF00041; En3; 3.
PFam; PF03228; Lep receptor_Ig; 1.
PROSITE; PS500851; EN3; 5.
PROSITE; PS01352; HEMATopo_REC_L_F2; 1.
3D-structure; Alternative_splicing; Direct_protein_sequencing;
Glycoprotein; Immunoglobulin_domain; Receptor; Repeat; Signal;
transmembrane.
SIGNAL 1 22 Interleukin-6 receptor beta chain.
CHAIN 23 918 Extracellular (Potential).
DOMAIN 23 619 Potentail.
TRANSMEM 620 641 Cyttoplasmic (Potential).
DOMAIN 642 918 19-like C2-type.
DOMAIN 125 216 Fibronectin type-III 1.
DOMAIN 222 321 Fibronectin type-III 2.
DOMAIN 326 418 Fibronectin type-III 3.
DOMAIN 423 514 Fibronectin type-III 4.
DOMAIN 518 610 Fibronectin type-III 5.
DOMAIN 725 755 Ser-rich.
SITE 310 314 WSXWS motif.
SITE 651 659 Box 1 motif.
DISULFID 28 54
DISULFID 48 103
DISULFID 134 144
DISULFID 172 182
CARBONYD 458 466
CARBONYD 458 466
CARBONYD -83 43 N-linked (GlcNAc. . .).
CARBONYD -83 83 N-linked (GlcNAc. . .).
CARBONYD 131 131 N-linked (GlcNAc. . .).
CARBONYD 157 157 N-linked (GlcNAc. . .).
CARBONYD 227 227 N-linked (GlcNAc. . .).
CARBONYD 379 379 N-linked (GlcNAc. . .).
CARBONYD 383 383 N-linked (GlcNAc. . .).
CARBONYD 553 553 N-linked (GlcNAc. . .).
CARBONYD 564 564 N-linked (GlcNAc. . .).
CARBONYD 325 329 RPSKA -> NIASF (in isoform 2).
VARSPLIC 330 918 /FTId=vSP_001684.
VARSPLIC 330 918 Missing (in isoform 2).
VARSPLIC 330 918 /FTId=vSP_001685.
STRAND 29 32
STRAND 37 39
TURN 40 41
STRAND 44 50
HELIx 52 58
TURN 59 59
HELIx 62 64
STRAND 65 69
TURN 70 71
STRAND 72 73
HELIX 76 83
STRAND 80 85
TURN 84 91
STRAND 86 91
STRAND 98 107
FT 108 110
FT 111 123
FT 130 137
FT 138 139
FT 143 147
FT 157 164
FT 165 166
FT 167 168
FT 172 173
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FT 264 265
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FT 274 277
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FT 291 292
FT 294 303
FT 304 305
FT 317 320
SEQUENCE 918 AA; 103
Query Match 9 ITSTANKIVWSDEP
Best Local Similarity 11
Matches 25; Conservativ
Db 82 INRTASSVTFIDIA
Qy 68 ACVIMPENOSIRT
Db 133 SCIV - NEGKQRC
Qy 9 ITSTANKIVWSDEP
Db 82 INRTASSVTFIDIA
Qy 68 ACVIMPENOSIRT
Db 133 SCIV - NEGKQRC
RESULT 4 Q26645 PRELIMINARY
AC Q26645 PRELIMINARY
DT 01-NOV-1996 (TREMBLrel.
DT 01-NOV-1996 (TREMBLrel.
DT 01-MAR-2004 (TREMBLrel.
DE ETS homologue.
GN Name=ETS homologue;
OS Stronylo-locutrotus purp
OC Eukaryota; Metazoa; Ech
OC Echinoidea; Euechinoide
OC Stronylo-locutrotus.
NCBI_TaxID=7668; OX RN [1]
SEQUENCE FROM N.A.
TISvSP=Embryonic;
RC Rao S.K.; Childs G.;
RA Submitted (JUN-1993) to
RL CC -I- SIMILARITY: Belongs
EMBL; L15417; ALA30048.
DR HSSP P27577; 1K79.

DR	GO:0005634; C:nucleus; IEA.	SQ	SEQUENCE	667 AA;	73612 MW;	B1D05DE90D60532C CRC64;
DR	GO:0003700; P:transcription factor activity; IEA.		Query Match	11.8%; Score 78.5;	DB 2;	Length 667;
DR	GO:0006355; P:regulation of transcription, DNA-dependent; IEA.		Best Local Similarity	24.8%; Pred. No. 41;		
InterPro	IPR000418; Ets.		Matches	22; Mismatches	53;	Indels 31; Gaps 6;
InterPro	IPR02341; HSP_ETS.	Qy	2 ANKPMQPIT-----STANAKIVWSDFTRLSTFSASLILQRQVKVGAELNNVSGQYVSVY 55			
InterPro	IPR010933; SAM_homology.	Db	420 ANSTIMQVATAINEMASTAEVARNTNTVSNTNATVAADQSK--RAVNKAYDTSVALLM 476			
InterPro	IPR003118; SAM_PNT.	Qy	56 KRPAPKPGCADACVIMPENQSRITYVIS-----GSAENLATKAWEETHKRNVDTFLFAS 110			
InterPro	IPR000398; Wing_hlx_DNA_bnd	Db	477 TOLETASENVTE---MSNETQKISTVINVIRIDIAEQTNLLALNATEAAAR-----A 524			
Pfam	PF00178; Ets_1.	Qy	111 GNGLGFIDPFTAIVSSPTTA 131			
PRINTS	PR00454; ETS_DOMAIN.	Db	525 GDQGRGF----AWADEVRA 540			
SMART	SM00413; ETS_1.					
SMART	SM00251; SAM_PNT.					
PROSITE	PS00345; ETS_DOMAIN_1; 1.					
PROSITE	PS00346; ETS_DOMAIN_2; 1.					
PROSITE	PS00061; ETS_DOMAIN_3; 1.					
DNA-binding; Nuclear_protein; DNA-binding; Nuclear protein; DNA-binding; Nuclease; Deinococcus; Deinococcales; Deinococcaceae; Deinococcus.	SEQUENCE 559 AA; 62052 MW;	SQ	SEQUENCE FROM N.A.			
CRC64;			RESULT 6			
Best Local Similarity	25.5%; Pred. No. 33;		Q9RT24 PRELIMINARY;			
Matches	40; Conservative 27; Mismatches 51; Indels 39; Gaps 7;		ID Q9RT24			
Qy	2 ANKPMQ---PITSTANKTWSDP-----TRLSTTFESASLILQRQVKVGAELNNVSGQYVS 53		AC Q9RT24;			
Db	208 ANVAQASSSSTSSTSSSSSTASPPVSVTTTTASSSSLSQSK-----LEVNSSGYLN 262		DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
Qy	54 V-----YKR-----YKRPEGCADACVIMPENQSRITYVIS-----GSAENLATKAWEETHKRNVDTFLFAS 91		DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
Db	263 TTSCMPRLDFLAGFESVNPQAVPVSACQCSGFSQDGS--MYQYSESTQLNBENABDIL 319		DE Malonyl CoA-acyl carrier protein transacylase.			
Qy	92 TLKAEWETHKRNVDTFLFAGNAGHGFDPAAIVSS 127		GN OrderedLocusNames:DR1345;			
Db	320 NIQEDTGGSSSDYVSLESSPNSNQHFFLETPTPETLYNN 356		OS Deinococcus radiodurans.			
			OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.			
			OC NCBI_TaxID:1299;			
		RN	OX			
		RP	SEQUENCE FROM N.A.			
		RC	STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;			
		RX	MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;			
		RA	White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vanathavan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.B., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.", Science 286:1571-1577(1999).			
		DR	DR ENBL; AE002033; AAF11497.1; -.			
		DR	FIR; AT5334; A75334.			
		DR	HSSP; P25715; IMPLA.			
		DR	TIGR; DR1945; -			
		DR	GO:0016740; F:transferase activity; IFA.			
		DR	GO: GO:0004314; F:[acyl-]carrier protein S-malonyltransferase. . . IEA.			
		DR	GO: GO:0006533; P:fatty acid biosynthesis; IEA.			
		DR	GO: GO:0008152; P:metabolism; IEA.			
		DR	InterPro; IPR01227; Ac transferase.			
		DR	InterPro; IPR004410; FabD.			
		DR	Pfam; PF00698; Acyl_transf_1; 1.			
		DR	TIGRFAM; TIGR00128; FabD; 1.			
		KW	Complete proteome.			
		SQ	SEQUENCE 305 AA; 31284 MW; 0564188B9FA35E9F CRC64;			
			Query Match	11.7%; Score 78;	DB 2;	Length 305;
			Best Local Similarity	28.9%; Pred. No. 18;		
			Matches	14; Mismatches	62;	Indels 10; Gaps 4;
		Qy	13 ANKIVWSDFTRLSTFSASLILQRQVKVGAELNNVSGQYVSVYKRAPKPEGC-ADACYI 71			
		Db	103 AGVLTLEDALRL-TRKGELMQDQAPVEGVGAMSAMGD-----PAVVAEVCAAQAGYV 154			
		Qy	72 MP-NENQSIRTVISGSAENLATKAWEETHKRNVDTFLASGNQGLGFLDPTAIVSSDT 130			
		Db	155 QPANFNAPQTIVSKEAVDAASELTRGLKAIPLKVSAAPHCALMRPAAEGLSAELH 214			
		KW	Complete proteome; Hypothetical protein.			

Qy	131 A 131 Db	215 A 215	Best Local Similarity 36.1%; Pred. No. 7.2e+02; Matches 35; Conservative 10; Mismatches 42; Indels 10; Gaps 4;
RESULT 7			
Q93HJ5	PRELIMINARY;	PRT;	6146 AA.
AC	[1]		
DT	01-DEC-2001 (TREMBrel. 19, Created)		
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)		
DT	25-OCT-2004 (TREMBrel. 28, Last annotation update)		
DE	Modular polyketide synthase.		
GN	Name=oInAl; OrderedLocusNames=SAV2899;		
OS	Streptomyces avermitilis.		
OC	Bacteria; Actinobacteria; Actinomycetales;		
OC	Streptomycineae; Streptomyctaceae; Streptomyces.		
OX	NCBI_TaxID=33903;		
RN	[1]		
SEQUENCE FROM N.A.			
STRAIN=NA-4680;			
RX	MEDLINE-200433198; PubMed=1572948; DOI=10.1073/pnas.211433198;		
RA	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonee T., RA		
RA	RA		
RA	RA		
RA	RA		
RT	"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites."		
RT	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-22608306; PubMed=12692562;		
RA	Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;		
RT	"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."		
RL	Nat. Biotechnol. 21:526-531 (2003).		
DR	EMBL; AB07940; BAB69192.1; ..		
DR	HSSP; P66033; Bac70610.1; ..		
DR	IPR006508; P:protease and peptidolysis; IEA.		
DR	IPR006508; P:peptidase activity; IEA.		
DR	IPR006508; P:subtilase activity; IEA.		
DR	IPR006508; Peptidase activity; IEA.		
DR	IPR006508; Prot_inh_S8A.		
DR	InterPro: IPR000209; Pept_S8_S33.		
DR	InterPro: IPR009020; Prot_inh_propept.		
DR	InterPro: IPR010259; Prot_inh_S8A.		
DR	PFam: PF00082; Peptidase_S8; ..		
DR	PFam: PF05922; Subtilisin_N; ..		
DR	PRINTS: PRO00723; SUBTILISIN.		
DR	PROSITE; PS00137; SUBTILASE_HIS; ..		
DR	PROSITE; PS00138; SUBTILASE_SER; ..		
KW	Complete proteome; Hydrolase; Protease; Serine protease.		
SQ	SEQUENCE 1454 AA; 155494 MW; 9223ADF205DD77FF CRC64;		
RESULT 8			
Q8ENZ2	PRELIMINARY;	PRT;	1454 AA.
ID	Q8ENZ2;		
AC	[1]		
DT	01-MAR-2003 (TREMBrel. 23, Created)		
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)		
DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)		
DE	Bacillopeptidase F (EC 3.4.21.-).		
GN	OrderedLocusName=OB2331;		
OS	Oceanobacillus iheyensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.		
OC	NCBI_TaxID=182710;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=HTB831;		
RX	Medline=2220767; PubMed=12235316; DOI=10.1093/nar/gkf526;		
RA	RA		
RT	Takami H., Takaki Y., Uchiyama T.		
RT	"Genome sequence of Oceanobacillus iheyensis isolated from the Ridge environment and its unexpected adaptive capabilities to extreme environments".		
RT	Nucleic Acids Res. 30:3927-3935 (2002).		
RL	-I- SIMILARITY: Belongs to peptidase family S8.		
CC	-I- SIMILARITY: Belongs to peptidase family S8.		
DR	EMBL; AP004600; BAC14287.1; ..		
DR	HSSP; Q99405; IMPT.		
DR	MEPROPS; S08..017; ..		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:004389; F:subtilase activity; IEA.		
DR	GO; GO:006508; P:protease and peptidolysis; IEA.		
DR	InterPro: IPR000209; Pept_S8_S33.		
DR	InterPro: IPR009020; Prot_inh_IMPT.		
DR	InterPro: IPR010259; Prot_inh_S8A.		
DR	PFam: PF00082; Peptidase_S8; ..		
DR	PFam: PF05922; Subtilisin_N; ..		
DR	PRINTS: PRO00723; SUBTILISIN.		
DR	PROSITE; PS00137; SUBTILASE_HIS; ..		
DR	PROSITE; PS00138; SUBTILASE_SER; ..		
KW	Complete proteome; Hydrolase; Protease; Serine protease.		
SQ	SEQUENCE 1454 AA; 155494 MW; 9223ADF205DD77FF CRC64;		
Query Match			
Qy	11.6%; Score 77.5; DB 2; Length 1454;		
Best Local Similarity 29.4%; Pred. No. 1.4e+02;			
Matches 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;			
DR	165 VNGIAVATKKVAKVTAEYKVAEWTKAEWETHKRNYDT 106		
DR	165 VNGIAVATKKVAKVTAEYKVAEWTKAEWETHKRNYDT 106		
Qy	47 VSGOYVSYKRPAPKPGCADACVIMDNEQSIIRTIVSGSAENLATKAEWETHKRNYDT 131		
DR	107 LFASGNAGLGFLDPAAIVSSDTA 221		
DR	107 LFASGNAGLGFLDPAAIVSSDTA 221		
DB	222 VGPATNNMGFDGSGVVVASIDTGA 246		
RESULT 9			
Q74KV6	PRELIMINARY;	PRT;	373 AA.
ID	Q74KV6;		
AC	AC		
DT	05-JUL-2004 (TREMBrel. 27, Created)		
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)		
DE	DNA_polymerase_IV.		
GN	OrderedLocusName=LuJ0471;		
Query Match	11.7%; Score 78; DB 2; Length 6146;		

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC	Chromataceae; Allochromatium.
OX	NCBI_TaxID=1049;
RN	SEQUENCE FROM N.A. MEDLINE=93188721; PubMed=8444812;
RX	"Cloning, characterization, and functional expression in Escherichia coli of chaperonin (groESL) genes from the phototrophic sulfur bacterium Chromatium vinosum.";
RA	Ferreira R., Soncini F., Viale A.M.;
RT	CHARACTERIZATION.
RX	MEDLINE=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;
RA	Dionisi H.M., Viale A.M.;
RT	GroES proteins overexpressed in Escherichia coli cells lacking the endogenous groESL operon.;"
RT	Purif. 14:275-282 (1998).
RL	-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions.
CC	-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits.
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.
CC	-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	DR EMBL; M99443; AAA23319.1; -;
DR	PTR; B47073; B47073.
HSPP	PG6139; 1G5S.
DR	HAMAP; MF_00600; -; 1.
DR	InterPro; IPR001844; Chaperonin_Cpn60.
DR	InterPro; IPR002423; Cpn60_TCP-1.
DR	InterPro; IPR008930; GroEL_ATPase.
PFAM	Pf001118; Cpn60_TCP1; 1.
PRINTS	PR00298; CHAPERONIN0.
PRINTS	PR00304; TCOMPLEXTCPI.
DR	PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW	ATP-binding; Chaperone.
SEQUENCE	546 AA; 57541 MW; 3250141881CO4DD6 CRC54;
SQ	DR 11.5%; Score 76.5; DB 1; Length 546; Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps 3;
RESULT 14	QTWS88 PRELIMINARY; PRT; 538 AA.
QY	3 NKPQPISTANKI--WSDPTTRLSTSASLLRQRYVKGIABL-----NVS 48
Db	68 NMGAQMVKVEASKTSIDAGDTTATVLAQMTRYREGKAVARGMNPMDLKGRMDKAVEAA 127
QY	49 GQYVSVYKPKPDKEGADACVMPNENGSIRTYSGEANL---ATTKAWEETHKND 105
Db	128 TBEIKKLSPKCPRMIAQVGTISANSDDSIGTIAEAMKEVKGREGVITVEDGTSLQNL 187
QY	106 TLFASGNAGLGFLDP 120
Db	188 DVYEGMQFFRGYLSP 202
RESULT 13	QT4BT9 PRELIMINARY; PRT; 436 AA.
ID	Q74BT9
AC	Q74BT9
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
RT	"A Novel Tetrahydrofolate-Dependent O-Demethylase Gene Is Essential for Growth of Sphingomonas paucimobilis SYK-6 with Syringate.";
DE	GGDEF domain/HAMP domain protein.
GN	OrderedLocusNames=GSU1937;
OS	Geobacter sulfurreducens.
OC	Geobacteraceae; Geobacter.
NCBI_TaxID=35554;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=PCA / ATCC 51573; PMID=14671304; DOI=10.1126/science.1088727;
RX	RA Methe B.A., Nelson K.E., Elsen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Graw M.L., Kollaray J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., RA Van Aken S.B., Lovley D.R., Fraser C.M.; RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface environments"; RT Science. 302:1967-1969(2003); RL EMBL; AE017180; AAR35313.1; -.
DR	DR TIGR; GSU1937; -;
DR	DR GO; GO:0016020; C:membrane; IEA.
DR	DR GO:0004871; F:signal transducer activity; IEA.
DR	DR GO:0007165; P:signal transduction; IEA.
DR	DR InterPro; IPR00160; GGDEF
DR	DR InterPro; IPR03660; His_kin_HAMP.
DR	DR PFAM; PF00930; GGDEF; 1.
DR	DR PFAM; PF00672; HAMP; 1.
DR	DR SMART; SM00267; DUF1; 1.
DR	DR SMART; SM00304; HAMP; 1.
DR	DR PROSITE; PS00887; GGDEF; 1.
DR	DR PROSITE; PS50885; HAMP; 1.
KW	Complete proteome.
SQ	SEQUENCE 436 AA; 48221 MW; FDRCBB6E7DF83400 CRC64;
Query Match	11.4%; Score 76; DB 2; Length 436;
Best Local Similarity	23.8%; Pred. No. 44;
Matches	30; Conservative 28; Mismatches 40; Indels 28; Gaps 6;
QY	12 TANKIVNSDPTRLSTFSASLLRQRYVKGIABLNNSGQQYYSVYKRPKPGCADACVI 71
Db	42 TAKREIARTDLFVTSATY-----RRESLSAQDRFAGRYL-ILK-----SDFRKD 84
QY	72 MPDENQS-LRTVIS----GSAENLATKAKAEWTHKRNVDTLFASGNGLGFIDPTAIV 125
Db	85 LENIQRSQEFMTILGELEGRGNDQPFRDIVASRYRQATESIFATGNG----DPLAAKK 139
QY	126 SSPTTA 131
Db	140 DSDEVA 145
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SYK-6;
RX	PubMed=1509517; DOI=10.1128/JB.186.9.2757-2765.2004;
RA	Masai B., Sasaki M., Minakawa Y., Abe T., Sonoki T., Miyauchi K., Katayama Y., Fukuda M.;
RT	"A Novel Tetrahydrofolate-Dependent O-Demethylase Gene Is Essential for Growth of Sphingomonas paucimobilis SYK-6 with Syringate.";

	SQ	SEQUENCE	540 AA;	60340 MW;	BCA8B2CBE127046P CRC64;
RL	J. Bacteriol.	186:2757-2765(2004).			
RP	[2]	SEQUENCE FROM N.A.			
RC	STRAIN=SYK-6;				
RX	MEDLINE=22188250; PubMed=12200295;				
RX	DOI=10.1128/AEM.6.9.4416-4424.2002;				
RA	Masai E., Harada K., Peng X., Kitayama H., Katayama Y., Fukuda M.;				
RT	"Cloning and characterization of the ferulic acid catabolic genes of				
RT	Sphingomonas paucimobilis SYK-6.".				
RL	Appl. Environ. Microbiol.	68:4416-4424(2002).			
CC	"SIMILARITY: Belongs to the TPP enzyme Family.				
DR	EMBL; AB110975; BAC79260.1. -.				
DR	HSSPC; P70342; 1U5C.				
DR	InterPro; IPR000339; Pyruvate decarb.				
DR	Pfam; PF00205; TPP enzyme N. 1.				
DR	PROSITE; PS00187; TPP_ENZYME; 1.				
KW	Hypothetical protein.				
SQ	SEQUENCE 538 AA; 56498 MW; EFFE92E0EEF305CB CRC64;				
Query Match	11.4%;	Score 76 DB 2; Length 538;			
Best Local Similarity	27.9%;	Pred. No. 57;			
Matches	43; Conservative 15; Mismatches 50; Indels 46; Gaps 9;				
Qy	5 PMQPITSTANKIYWSDPTRLSTPSASLURQRYVGIAELNNVSGQY--VSYYKRPAKP 62				
Db	298 PYVEGAGSIV-DDPS-----ENLATIKA-----WETH- 100				
Qy	63 EGGADACVIMPENQSIIRTIVSGA-----ENLATIKA-----WETH- 100				
Db	346 RAVFDAALAPN-----WVGSGTAIEELLMQQLATLRPKGTTISSEAPSTRGPMDHF 399				
Qy	101 -KRNDTLPASGNGLGFDP-----AAIVSSDFT 130				
Db	400 PIRLEDFMATAASCGLGPALPAAVGAATIQPDRT 433				
SEARCH completed: June 1, 2005, 09:45:53					
Job time : 117 secs					
RESULT 15					
Q7SG34	PRELIMINARY;	PRT;	540 AA.		
ID	Q7SG34				
AC	Q7SG34;				
DT	01-MAR-2004 (TREMBBrel. 26, Created)				
DT	01-MAR-2004 (TREMBBrel. 26, Last sequence update)				
DT	01-MAR-2004 (TREMBBrel. 26, Last annotation update)				
DB	Predicted Protein.				
GN	Name=NC07508.1;				
OS	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.				
NCBI_TaxID	=5141;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=OR74A;				
RA	Galagan J.E., Calvo S.B., Borkovich K.A., Selker E.U., Read N.D.,				
RA	Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,				
RA	Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,				
RA	Qui D., Ianakiev P., Pedersen D., Nelson M., Washburn M.,				
RA	Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,				
RA	Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,				
RA	Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,				
RA	Kamal M., Kamvysseis M., Mauceli E., Bielek C., Rudd S., Frishman D.,				
RA	Kryftofova S., Ratanusorn C., Metzenberg R.L., Perkins D.D., Kroken S.,				
RA	Cogoni C., Macino G., Catchpole D., Li W., Pratt R.J., Osman S.A.,				
RA	DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,				
RA	Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,				
RA	Natvig D.O., Alex L.A., Mamhaup G., Ebbole D.J., Freitag M.,				
RA	Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,				
RT	"The Genome Sequence of the Filamentous Fungus Neurospora crassa."				
RL	Nature 0:0-0(2003).				
CC	- CAUTION: The sequence shown here is derived from an				
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is				
DR	preliminary data.				
CC	ABX01000013; EAA35819.1; -.				

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Om protein - protein search, using sw model

Run on: June 1, 2005, 09:34:17 ; Search time 114 Seconds
 (without alignments)
 588.442 Million cell updates/sec

Title: US-10-617-876-3
 Perfect score: 666
 Sequence: 1 MANKTMQPITSTANKIVWSD.....NAGLGFELDPTAAIVSDDTTA 131

Scoring table: BLASTM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03-*
 1: uniprot_sprot:/*
 2: uniprot_trembl:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	660	99.1	131	2	Q9AZ42	Q9az42 bacteriophaga
2	84.5	12.7	667	2	Q6LQF7	Q6lqf7 photobacter
3	80	12.0	194	1	LPPK MYCLE	Q43803 mycobacteri
4	79	11.9	918	1	IL6B HUMAN	P40189 homo sapien
5	78	11.7	305	2	Q9RTZ4	Q9rtz4 deinococcus
6	78	11.7	524	2	042147	042147 xenopus lae
7	78	11.7	524	2	Q8AVN9	Q8avn9 xenopus lae
8	78	11.7	6146	2	093HAT5	Q93hj5 streptomyce
9	77.5	11.6	1174	2	Q8MPRO	Q8mpo crassostrea
10	77.5	11.6	1454	2	QBENZ2	Q8enz2 oceanobacil
11	77	11.6	373	2	Q7AKV6	Q7akv6 lactobacill
12	77	11.6	1088	2	Q6ZDUR6	Q6zdu6 homo sapien
13	76.5	11.5	457	2	Q6C3PF9	Q6c3pf9 yarrowia li
14	76	11.5	546	1	CH60 CHRV1	P31293 chromatium
15	76.5	11.5	988	2	Q87ID1	Q87id1 vibrio para
16	76	11.4	436	2	Q74BT9	Q74bt9 geobacter s
17	75.5	11.3	519	1	ACHG BOVIN	P13536 bos taurinus
18	75	11.3	538	2	Q7WSS8	Q7wss8 pseudomonas
19	75	11.3	386	2	Q8P9T4	Q8pt4 xanthomonas
20	75	11.3	711	2	Q6MKR4	Q6mk4 bdellovibrri
21	75	11.3	881	2	Q7RM96	Q7rm96 plasmidium
22	74	11.1	559	2	Q26645	Q26645 stronglyloce
23	74	11.1	620	2	Q12623	Q12623 humicola gr
24	74	11.1	713	2	Q8EV63	Q8ev63 mycoplasma
25	74	11.1	1084	2	Q6BGK7	Q6bgk7 paramaecium
26	74	11.1	1693	2	Q7RLG9	Q7rlg9 plasmidium
27	74	11.1	1851	2	Q8JUF5	Q8ju5 bean pod mo
28	74	11.1	2799	1	G112 HUMAN	Q81zf6 homo sapien
29	73.5	11.0	213	2	Q50402	Q50402 mycobacteri
30	73.5	11.0	291	2	Q9SBF9	Q9sbf9 arabiopsis
31	73.5	11.0	296	2	Q7WNL6	Q7wnl6 mycobacteri

ALIGNMENTS

RESULT 1									
QA242		PRELIMINARY;		PRT;		131 AA.			
ID	QA242;	AC	QA242;	DT	01-JUN-2001 (TREMBLrel. 17, Created)	DR	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	DR	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DB	Coat protein.	OS	Bacteriophage AP05.	OS	Virus; ssRNA positive-strand viruses, no DNA stage; Leviviridae; Levivirus.	NCBI	NCBI TAXID=154784;	NCI	SEQUENCE FROM N.A.
RN		RA	Kloving J.; Overbeek G.P., van Duin J.; Ackermann H.W., van Duin J.; "Nucleotide sequence of a ssRNA phage from Acinetobacter: kinship to coliphages"; J. Gen. Virol. 83:1523-1533 (2002).	RA	Kloving J.; Overbeek G.P., van Duin J.; Ackermann H.W., van Duin J.; "Nucleotide sequence of a ssRNA phage from Acinetobacter: kinship to coliphages"; J. Gen. Virol. 83:1523-1533 (2002).	RA	Kloving J.; Overbeek G.P., van Duin J.; Ackermann H.W., van Duin J.; "Nucleotide sequence of a ssRNA phage from Acinetobacter: kinship to coliphages"; J. Gen. Virol. 83:1523-1533 (2002).	RA	SEQUENCE FROM N.A.
RP		RP	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.	RP	RP	RP	RP	RP	RP
YQ	1 MANKTMQPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 60	Db	1 MANKTMQPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 60	Db	1 MANKTMQPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 60	Db	1 MANKTMQPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 60	Db	1 MANKTMQPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 60
YQ	1 MANXKIPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 120	Db	1 MANXKIPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 120	Db	1 MANXKIPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 120	Db	1 MANXKIPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 120	Db	1 MANXKIPITSTANKIVWSDPTRLSTSASLIRQVRKGIAINNYSGQQYXSVYKRCPAP 120
YQ	1 TAAIVSSDTTA 131	Db	1 TAAIVSSDTTA 131	Db	1 TAAIVSSDTTA 131	Db	1 TAAIVSSDTTA 131	Db	1 TAAIVSSDTTA 131

RESULT 2

Q6LQF7 PRELIMINARY; PRT; 667 AA.

AC Q6LQF7; DT 05-JUL-2004 (TREMBLrel. 27, Created)

DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE	Hypothetical 1 methyl-accepting chemotaxis protein.
GN	Name=PSPT0323; OrderedLocusNames=PPRA2077;
OS	Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibriionales;
OC	Vibrionaceae; Photobacterium.
OX	NCBI_TaxID=74109;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	VEZZI A., CARPANARO S., D'ANGELO M., SIMONATO F., VITULO N., LAURO F., CESTARI A., MALACRIDA G., SIMIONATI B., CANNATA N., BARTLETT D., VALLE G.
RA	"Genome analysis of Photobacterium profundum reveals the complexity of high pressure adaptations." RT
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: CB378659; CAG20479_1. -
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0004877; F:signal transducer activity; IEA.
DR	GO; GO:0006935; P:chemotaxis; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	InterPro; IPR004089; Chmtaxis transl.
DR	DR InterPro; IPR003660; His kin. HAMP.
DR	InterPro; IPR00727; T_SNARE.
DR	Pfam; PF00672; HAMP; 1.
DR	Pfam; PF00015; MCPB signal; 1.
DR	SMART; SM00304; HAMP; 1.
DR	SMART; SM0023; MA_1.
DR	PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2;
DR	PROSITE; PS50885; HAMP; 1.
DR	PROSITE; PS50192; T_SNARE; 1.
RW	Complete sequence; Hypothetical protein.
SQ	SEQUENCE 667 AA; 73612 MW; B105D9E90D60532C CRC64;
Query	Match 12.7%; Score 84.5; DB 2; Length 667;
Best Local Similarity 25.5%; Pred. No. 10;	
Matches 36; Conservative 22; Mismatches 52; Indels 31; Gaps 5	
Qy	2 ANKTMQPI-----STANKIVWSDFTRLSPTFSALLRQVRVGLABLNNSGQTVSVY 5
Db	420 ANETMQVTAINEAMASTAEVARNTNTVNTNTHNAYADOSK--AVVNKAFTDSVALLM 4
Qy	56 KRAPKPEGGADACVIMPENQNSIRIVS---GSAENLTAKAEAEHTKRNVDTLFAS 1
Db	477 TQIETASENTE---MSNETQKISTVLNVRDIAEQTNLLALNAAEAAAR-----A 5
Qy	111 GNAGIGFLDPTAIVSSDTA 131
Db	525 GDQGRGF----AVVADEVRA 540
RESULT 3	LPPK_MYCLE STANDARD PRT; 194 AA.
ID	LPPK_MYCLE
AC	Q9803;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Purative lipoprotein lppK precursor.
Name	=lppK; OrderedLocusNames=MLC2533_11c;
GN	ORFNames=MLC2533_11c; B2126_F3_115;
OS	Mycobacterium leprae.
OC	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX	NCBI_TaxID=1789;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	SMITH D.R., ROBISON K.; Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RL	SEQUENCE FROM N.A.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Tn;
RX	Medline=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA	Cole S.T., Eiglemeier K., Parikh J.J., James K.D., Thomson N.R., Wieseler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., RA

RN	[2]	SEQUENCE FROM N.A. (ISOFORM 2).
RP	TISSUE=Synovium;	P:cell surface receptor linked signal transdu. . . ; TAS.
RC	RC	GO; GO:0006555; P:immune response; TAS.
RX	Medline2031529; PubMed=10800801; DOI=10.1093/jbc.M009979200;	InterPro; IPR0202996; CytkN_recept_B/G.
RA	Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M., Murakami M., Nakao K.;	DR DR DR DR DR DR
RA	"Cloning of novel soluble gp130 and detection of its neutralizing autoantibodies in rheumatoid arthritis.";	IPRO03961; FN_III-like. IPRO08957; FN_III-like. IPRO03529; Hemptrecept_1302. IPR010457; Lep_receptor_Ig.
RT	J. Clin. Invest. 106:137-144 (2000).	PFam; PF00041; fn3; 3. PFam; PF00328; Lep_receptor_Ig; 1.
RN	[3]	PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX	Medline21269388; PubMed=11098061; DOI=10.1074/jbc.M009979200;	DR PROSITE; PS08053; FN3; 5.
RA	Bravo J., Hall N.E., Connolly L.M., Simpson R.J.;	DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
RT	"Determination of the disulfide structure and N-glycosylation sites of the extracellular domain of the human signal transducer gp130.";	KW 3D-structure; Alternative splicing; Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal; Transmembrane.
RT	J. Biol. Chem. 276:8244-8253 (2001).	KW SIGNAL 1
RN	[4]	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RP	Medline98163983; PubMed=951088; DOI=10.1093/embj/17.6.1665;	FT DOMAIN 22
RX	Bravo J., Staunton D., Heath J.K., Jones B.Y.;	FT TRANSMEM 23
RA	"Crystal structure of a cytokine-binding region of gp130.";	FT DOMAIN 23
RT	ENBO J. 17:1665-1674 (1998).	FT DOMAIN 620
-!	FUNCTION: Signal-transducing molecule. The receptor systems for IL6, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating signal transmission. Binds to IL6/IL6R (alpha chain) complex, resulting in the formation of high-affinity IL6 binding sites, and transduces the signal. Does not bind IL6. May have a role in embryonic development (By similarity).	FT DOMAIN 641
CC	SUBUNIT: Heterodimer of an alpha and a beta chain.	Cytoplasmic (Potential).
-!	SUBCELLULAR LOCATION: Type I membrane protein (isoform 1). Secreted (isoform 2).	FT DOMAIN 918
CC	-	IG-like C2-type.
-!	ALTERNATIVE PRODUCTS:	Fibronectin type-III 1.
CC	Event=Alternative splicing; Named isoforms=2;	Fibronectin type-III 2.
CC	Name=1; IsoId=P40189-1; Sequence=Displayed;	Fibronectin type-III 3.
CC	Name=2; Synonyms=gp130-RAPS;	Fibronectin type-III 4.
CC	IsoId=P40189-2; Sequence=VSP 001684; VSP 001685;	Fibronectin type-III 5.
CC	-!	TRISSUE_SPECIFICITY: Found in all the tissues and cell lines examined. Expression not restricted to IL-6 responsive cells.
CC	-	DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
CC	-	DOMAIN: The box 1 motif is required for JAK interaction and/or activation.
CC	-	DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis (RA), but it is not specific to patients with RA.
CC	-	SIMILARITY: Belongs to the type I cytokine family of receptors.
CC	-	Subfamily 2.
CC	-!	SIMILARITY: Contains 5 fibronectin type III domains.
CC	-	SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC	-	DATABASE: NAME=PROW; NORB=CD Guide CD130 entry; www="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
CC	-	STRAND 30 918
CC	-	STRAND 29 32
CC	-	STRAND 37 39
CC	-	TURN 131 41
CC	-	STRAND 157 50
CC	-	CARBOHYD 227 73
CC	-	CARBOHYD 379 182
CC	-	CARBOHYD 433 466
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (GLCNAC. . .).
CC	-	N-Linked (VSP 001684. Missing (In isoform 2). /FTId=VSP_001685.
CC	-	/FTId=VSP_001685.
CC	-	STRAND 59 59
CC	-	STRAND 62 64
CC	-	STRAND 65 69
CC	-	TURN 70 71
CC	-	STRAND 72 73
CC	-	HELIX 76 78
CC	-	STRAND 80 83
CC	-	TURN 84 91
CC	-	STRAND 86 91
CC	-	TURN 98 107
CC	-	TURN 108 110
CC	-	STRAND 111 123
CC	-	STRAND 130 137
CC	-	TURN 138 139
CC	-	STRAND 143 147
CC	-	STRAND 157 164
CC	-	TURN 165 166
CC	-	STRAND 167 168
CC	-	STRAND 172 173
CC	-	TURN 179 180
CC	-	STRAND 181 183
CC	-	TURN 190 191

PT	STRAND	194	202	KW	Complete proteome.
PT	TURN	203	204	SQ	SEQUENCE 305 AA; 31284 MW; 0564188B9FA35E9F CRC64;
PT	STRAND	205	208	Query Match 11.7%; Score 78; DB 2; Length 305;	
PT	STRAND	212	214	Best Local Similarity 28.9%; Pred. No. 18;	
PT	HELIX	216	219	Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;	
PT	STRAND	220	221	Qy 13 ANKIVWSDPTRDSTFSASILRQRVKVIAELNNVSQYVSVYKRPAPKPEGG-ADACVI 71	
PT	STRAND	226	231	Db 103 AGVLTLEDALRL-TRKGEMLMQAVPREGVGAMSAMGD-----PAVVAEVCAAGVV 154	
PT	STRAND	240	245	Qy 72 MP-NENOSIRTVISGSAENLATIKAWEETHKVNVDTLFASGNAGLGFIDOPTAIVSSDTT 130	
PT	HELIX	248	251	Db 155 QPANFNAPQTOTVSGEKAADVAAASALIKTRGLKAIPLKVSAPFHCALMRPAEGSALH 214	
PT	TURN	252	252	Qy 131 A 131	
PT	STRAND	255	263	Db 215 A 215	
PT	TURN	264	265	RESULT 6	
PT	STRAND	270	271	Qy 103 ANKIVWSDPTRDSTFSASILRQRVKVIAELNNVSQYVSVYKRPAPKPEGG-ADACVI 71	
PT	HELIX	274	277	Db 103 AGVLTLEDALRL-TRKGEMLMQAVPREGVGAMSAMGD-----PAVVAEVCAAGVV 154	
PT	STRAND	283	286	Qy 72 MP-NENOSIRTVISGSAENLATIKAWEETHKVNVDTLFASGNAGLGFIDOPTAIVSSDTT 130	
PT	TURN	291	292	Db 155 QPANFNAPQTOTVSGEKAADVAAASALIKTRGLKAIPLKVSAPFHCALMRPAEGSALH 214	
PT	STRAND	294	303	Qy 131 A 131	
PT	TURN	304	305	Db 215 A 215	
PT	STRAND	317	320	RN [1] PRELIMINARY; PRT; 524 AA.	
SQ	SEQUENCE	918 AA;	103522 MW;	RN [1] PRELIMINARY; PRT; 524 AA.	
Query Match 11.9%; Score 79; DB 1; Length 918; Best Local Similarity 25.5%; Pred. No. 55; Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;	Q9RT24	PREDICTED	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Qy 9 ITSTANKIVWSDPTRDSTFSASILR-ORVKVIAELNNVSQYVSVYKRPAPKPEGGAD 67	ID	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Db 82 INRTASSVTFTDIASLNQTCNLITFGLEQNYGTTISG-----LPFPBKPKNL- 132	AC	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Qy 68 ACVYMPNENQSIIRTIVISGSAENLA---TLLKAWEETHK 101	DT	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Db 133 SCIV--NEGKMRCEBWDGGRETHLETNFLLKSEWATHK 168	DT	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
RESULT 5	Q9RT24	PREDICTED	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Q9RT24	ID	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
AC 01-MAY-2000 (TREMBrel. 13, Created)	AC	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)	DT	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DE 01-MAR-2004 (TREMBrel. 26, Last annotation update)	DE	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
GN Orderedocushnames:DR1945;	GN	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
OS Deinococcus radiodurans.	OS	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Bacteria; Deinococcaceae; Deinococci; Deinococcales;	NCBI_TaxID:1299;	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
Deinococci; Deinococcus-thermus; Deinococcus; Deinococcus;	NCBI_TaxID:1299;	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
OC Deinococciaceae; Deinococcus	NCBI_TaxID:1299;	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
OX Deinococcus	NCBI_TaxID:1299;	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
SEQUENCE FROM N.A.	RP	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
STRAIN=RI / ATCC / 13939 / DSM 20539 / NCIB 9279; MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571; RA White O., Eisen J. A., Heideberg J. F., Hickey B. K., Peterson J. D., Dodson R. J., Haft D. H., Gwin M. L., Nelson W. C., Richardson D. L., Moffat K. S., Qin H., Jiang L., Pamphil W., Crosby M., Shen M., Vanathavorn J. J., Lam P., McDonald L. A., Utterback T. R., Zalewski C., Makarova K. S., Aravind L., Daly M. J., Minton K. W., Fleischmann R. D., Keilum K. A., Nelson K. E., Salzberg S. L., Smith H. O., Venter J. C., Fraser C. M.; "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1." Science 286:1571-1577(1999).	RP	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
RT Science 286:1571-1577(1999); EMBL; AB02033; AF11497.1; PIR; A75334; A75334.	RT	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
HSRP; P25715; 1MLA.	RT	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DR GO: GO:0016740; Fitransferase activity; IEA.	RT	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DR GO: GO:0004314; Facyl-carrier protein] S-malonyltransferase. . . ; IEA.	DR	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DR GO: GO:006633; Fatty acid biosynthesis; IEA.	DR	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DR InterPro; IPRO004410; FabD.	DR	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DR Pfam; PF00698; Acyl transferase.	DR	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
DR TIGRFAMs; TIGR00128; fabD; 1.	DR	Q9RT24	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	
RESULT 7	QBAVN9	PREDICTED	PREDICTED	RN [1] PRELIMINARY; PRT; 524 AA.	

AC QBAVN9;	91	ATLKAEWETHKRNV-DTILFASGNAGLGFIDPTAAIV 125
DT 01-MAR-2003 (TREMBurel; 23; Created)	:	:
DT 01-MAR-2003 (TREMBurel; 23; Last sequence update)	:	:
DR Jaz-Prov protein.	259	SMTPLSBRGHQAVVAPSIAASGAGKGKPSCDTNIV 294
OS Xenopus laevis (African clawed frog).		
OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Xenopodinae; Xenopus.		
OX NCBI_TaxID=8355;		
RP SEQUENCE FROM N.A.		
RC TISSUE=embryo;	RESULT 8	
RX MEDLINE=222388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	Qy Q93HJ5	PRELIMINARY;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schulter G.D., Klausner R.D., Collings F.S., Wagner L., Schaeffer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Blatchley M., Marusina L., Farmer A.A., Rubin G.M., Hong L., Scaplehorn M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Loquellion N.A., Peters R.D., Abramson D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton R., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Smailus D.B., Butterfield Y.S., Jones S.J., Marras M.A./	Db Q93HJ5	PRT; 6146 AA.
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";		
RP PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).		
RL [2]		
RP SEQUENCE FROM N.A.		
RC TISSUE=embryo;		
RX MEDLINE=222341132; PubMed=12454917; DOI=10.1002/adv.10174;		
RA Klein S.L., Straubberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;		
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative.";		
RL Dev. Dyn. 225:384-391 (2002).		
RP SEQUENCE FROM N.A.		
RC Tissue=embryo;		
RL Submitted (DBIC-2002) to the EMBL/GenBank/DBJ databases.		
DR GO: GO:0041713; ARH41713; -.		
DR InterPro; IPR004534; C-nucleus; IEA.		
DR GO: GO:003676; F:nucleic acid binding; IEA.		
DR GO: GO:003676; F:zinc ion binding; IEA.		
DR GO: GO:0082710; F:zinc ion binding; IEA.		
DR InterPro; IPR00345; CytC_heme_BS.		
DR InterPro; IPR00707; Znf_C2H2.		
DR SMART; SM00355; Znf_C2H2.		
DR SMART; SM00451; Znf_CU_7.		
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.		
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN 7.		
SEQUENCE 524 AA; 55546 MW; B55736038AC13D5C CRC64;		
Query Match 2 ANKTMQPTISTA-NKIVSDPTRL---STTPSASL-----RQYVKVGIAEL 44		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Qy 91 ATLKAEWETHKRNV-DTILFASGNAGLGFIDPTAAIV 125		
Db 259 SMTPLSBRGHQAVVAPSIAASGAGKGKPSCDTNIV 294		
Qy 2 ANKTMQPTISTA-NKIVSDPTRL---STTPSASL-----RQYVKVGIAEL 44		
Db 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Qy 91 ATLKAEWETHKRNV-DTILFASGNAGLGFIDPTAAIV 125		
Db 259 SMTPLSBRGHQAVVAPSIAASGAGKGKPSCDTNIV 294		
Qy 2 ANKTMQPTISTA-NKIVSDPTRL---STTPSASL-----RQYVKVGIAEL 44		
Db 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 524;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Qy 91 ATLKAEWETHKRNV-DTILFASGNAGLGFIDPTAAIV 125		
Db 259 SMTPLSBRGHQAVVAPSIAASGAGKGKPSCDTNIV 294		
Qy 2 ANKTMQPTISTA-NKIVSDPTRL---STTPSASL-----RQYVKVGIAEL 44		
Db 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
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Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
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Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
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SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
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Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
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Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
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Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSGQTDPQAQPTPLNNSMPGSGSAGKFSCKCNVTLNSIEQYQAHVSAGKHNQML 258		
Query Match 11.7%; Score 78; DB 2; Length 6146;		
Best Local Similarity 26.9%; Pred. No. 35;		
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;		
SQ 139 AKTRTRPTATSKDNKDHSDRAKPCLUHSFTNNPLMAEQHYAGKHKQETKTQIMI 198		
Qy 45 NNYSGQYVSYVYKRP---APKP_EGCC-----DACYMPNENOSTRTVTSQSAEN---L 90		
Db 199 YTSSG		

Best Local Similarity 36.1%; Pred. No. 7.2e+02; Matches 35; Conservative 10; Mismatches 42; Indels 10; Gaps 4;	OS Oceanobacillus iheyensis.
Qy 24 LSTTSFASILRQRVTKVGLNLNNYSGQYSVYKRPAKPKEGCA---DACVIMPENQSI 79	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus . NCBITaxID=182710; [1]
Db 3100 LSLEDGAATLRSRL-IABELS3HGMVSVALSADTATERIARWNGTCVAANNSRRS- 3157	RN SEQUENCE FROM N.A.
Qy 80 RTVISGSAEMLATKAEME--THKRNVTDLFASGNA 113	RC STRAIN=TIE81;
Db 3158 -TVVSGEPEALAEELAECBAEGVRARRTIVDYASHA 3193	RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
	RA Takami H., Takaki Y., Uchiyama I..
	RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."
	RT Nucleic Acids Res. 30:3927-3935(2002).
	RL CC -I SIMILARITY: Belongs to peptidase family S8.
	DR EMBL; AP004600; BAC14287.1; -.
	DR HSSP; Q99405; IMP1.
	DR MEROPS; S08_017;
	DR GO; GO:0008233; P:peptidase activity; IEA.
	DR GO; GO:0004289; P:subtilase activity; IEA.
	DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
	DR InterPro; IPR00209; Pept_S8_S53.
	DR InterPro; IPR01020; Prot_inh_propept.
	DR InterPro; IPR010259; Prot_inh_SPA.
	DR Pfam; PF00082; Peptidase_S8; _.
	DR Pfam; PF05923; Subtilisin_N; 1.
	DR PRINTS; PR00723; SUBTILISIN.
	DR PROSITE; PS00137; SUBTILASE HIS; 1.
	DR PROSITE; PS00138; SUBTILASE SER; 1.
	KW Complete proteome; Hydrolase; Protease; Serine protease.
	SQ SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7P CRC64;
RESULT 9	Query Match Score 77.5; DB 2; Length 1454;
QBMPRO ID QBMPRO PRELIMINARY;	Best Local Similarity 29.4%; Prod. No. 1_4e+02; Indels 3; Gaps 1;
AC QBMPRO;	SEQUENCE 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)	QY 47 VSGOYVSYTKRPAKPKEGCADACTVIMPNENQSIIRTIVSGSAENLATKAEWETHKRNYDT 106
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DR GO; GO:0008233; P:peptidase activity; IEA.
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DE Bone morphogenic protein type 2 receptor.	DR InterPro; IPR00209; Pept_S8_S53.
GN Name=BMP-R2 gene;	DR InterPro; IPR01020; Prot_inh_propept.
GS Crassostrea gigas (Pacific oyster).	DR InterPro; IPR010259; Prot_inh_SPA.
GS Bivalvia; Metazoa; Mollusca; Bivalvia; Ostreida; Ostreoida; Ostreidae; Ostreidae; Crassostrea.	DR Pfam; PF00082; Peptidase_S8; _.
OX NCBI_TaxID=29159;	DR Pfam; PF05923; Subtilisin_N; 1.
OX NCBI_TaxID=29159;	DR PRINTS; PR00723; SUBTILISIN.
[1]	DR PROSITE; PS00137; SUBTILASE HIS; 1.
RP PROSITE; PS00138; SUBTILASE SER; 1.	DR PROSITE; PS00138; SUBTILASE SER; 1.
SEQUENCE FROM N.A.	KW Complete proteome; Hydrolase; Protease; Serine protease.
RA Herpin A.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.	SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7P CRC64;
EMBL; A427430; CD20574.1; -.	SQ SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7P CRC64;
HSSP; P46897; 1IAS	Query Match Score 29.4%; DB 2; Length 1454;
DR GO; GO:0005524; CAMP binding; IEA.	Best Local Similarity 29.4%; Prod. No. 1_4e+02; Indels 3; Gaps 1;
DR GO; GO:0004672; F-protein kinase activity; IEA.	Matches 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;
DR GO; GO:0007872; F-receptor activity; IEA.	QY 47 VSGOYVSYTKRPAKPKEGCADACTVIMPNENQSIIRTIVSGSAENLATKAEWETHKRNYDT 106
DR GO; GO:0005024; Transforming growth factor beta receptor ac. . ; IEA.	DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0006468; F-protein amino acid phosphorylation; IEA.	DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0017178; Transmembrane receptor protein serine/threon. . ; IEA.	DR InterPro; IPR00209; Pept_S8_S53.
DR InterPro; IPR00472; Activin receptor.	DR InterPro; IPR00033; Actn_receptorII.
DR InterPro; IPR01109; Kinase like.	DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR000719; Prot_Kinase.	DR InterPro; IPR00653; ACTIVIN2R.
DR PROSITE; PR00653; ACTIVIN2R.	DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.	KW
KW	RESULT 11
SEQUENCE 1174 AA; 132154 MW; 5E3928BD1406507A CRC64;	Q74KV6 PRELIMINARY; PRT; 373 AA.
QY 5 TMQPITSTANKI-TWSDPRLSTFSASILRQRYKVGIAE-----UNVSGQYV--- 52	ID Q74KV6 PRELIMINARY; PRT; 373 AA.
Db 686 TTPITTTTFSQFISSEPRHTPTTA-MAPTRBETGTADNSTASMVNISPNNGYITSR 744	AC Q74KV6 PRELIMINARY; PRT; 373 AA.
Qy 53 -SVTKRPAKPKPEG-CADACTVIM-PNENQS---IRTVISSAENLATK-----AEWE 98	DT 05-JUL-2004 (TREMBLrel. 27, Created)
Db 745 SSWTNRPGMTTSGSNTETVLMPSFSEDEAPPVYLNVNLAKNTVLPVHQGRPIABRN 804	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
Qy 99 THKRNVTDLFASGN 112	RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Scheill M.A.;
Db 805 THRSDEELSVSGN 818	RA "The genome sequence of the probiotic intestinal bacterium Lactobacillus Johnsonii NCC 533."
	RA DR Prok Natl Acad Sci U.S.A. 101:2512-2517 (2004).
	RA DR EMBL; AE017201; AAS08463.1; -.
	RA DR GO; GO:0006281; P:DNA repair; IEA.
	RA DR InterPro; IPR01126; UMUC_like.
RESULT 10	DR Pfam; PF00082; Peptidase_S8; _.
QBENZ2 ID QBENZ2 PRELIMINARY;	DR PROSITE; PSS0173; UMUC; 1.
AC QBENZ2;	DR PROSITE; PSS0173; UMUC; 1.
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	KW Complete proteome.
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	SEQUENCE 373 AA; 42240 MW; 3D2A1421FD195BE7 CRC64;
DE Bacillopeptidase F (EC 3.4.-.21.-.)	SQ OrderedLocusName=OB2331;

Query Match	11.6\$;	Score 77;	DB 2;	Length 373;		Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleylevasten C., Boisrame A., Boyer J., Cattolico L., Contaniolier F., de Daruvar A., Despins L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Pelizzetti S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpellini C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
Matches	21;	Best Local Similarity	27.6\$;	Pred. No. 29;		
Qy	12 TANKIIVSDFPTRLSTFSASLIRRORV--KVGIAE-----LNNVSQTVSYVKRPAF 60	Indels	25;	Indels 16;	Gaps 3;	
Db	124 TENKLNLTFPVRI----AALQQLERIYQIGLSSFGVSYNKFALKMSEYAKPFGRTVI 178					
Qy	61 KPEGADAACTVMPNEN 76					
Db	179 KPEGARDPLAKQPIKN 194					
RESULT 12						
Q6ZDM6	PRELIMINARY;	PRT;	1088 AA.			
AC	Q6ZDM6;					
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)					
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)					
DE	Hypothetical protein FLU43556.					
OS	Homo Sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
NCBI_TaxID	=9606;					
RN						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CLIB99;					
RA	GenoScope;					
RA	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; CR382131; CAG80411.1; GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IBA; InterPro; IPR007312; P:esterase; PFam; PF04185; Phosphoesterase_1.					
DR	Sequence 457 AA; 50001 MW;					
SO	523BB4A48FB34C4C CRC64;					
Query Match	11.5\$;	Score 76.5;	DB 2;	Length 457;		
Best Local Similarity	23.7\$;	Pred. No. 42;				
Matches	32;	Conservative 20;	Mismatches 34;	Indels 49;	Gaps 6;	
Qy	46 NVSQQTIVSYVKRPAKPGCADACVIMP-NENQ------SIRTIVSGSA----- 87					
Db	242 SVSGRYTNWVKPLNNTEFARDSLIIITFDENETYKDQNSVLAILLGGAVPDHRLRGTYD 301					
Qy	88 -----ENLATKAEN----- 116					
Db	302 DTFWDHSNLATEANWLPHLGRGDDVNANVFKEVADELNKRNISTEGLYHNASQPGY 361					
Qy	117 FLDPATAIVSSDTTA 131					
Db	362 FMDDTVPTIPVVDITA 376					
RESULT 14						
CH60_CHRV1	STANDARD;	PRT;	546 AA.			
ID	CH60_CHRV1					
AC	P31293;					
DT	01-JUL-1993 (Rel. 26, Created)					
DT	01-JUL-1993 (Rel. 26, Last sequence update)					
DE	05-JUL-2004 (Rel. 44, Last annotation update)					
GN	Name=groL; Synonyms=groEL, mopa;					
OS	Chromatium vinosum.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;					
OC	Chromatiaceae; Allochromatium.					
NCBI_TaxID	=1049;					
RN	SEQUENCE FROM N.A.					
RP	CHARACTERIZATION;					
RX	Medline=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;					
RX	Dionisi H.M., Viale A.M.;					
RA	Ferreira R., Soncini F., Viale A.M.;					
RT	"Cloning, characterization, and functional expression in Escherichia coli of chaperonin (groESL) genes from the phototrophic sulfur bacterium Chromatium vinosum."					
RT	J. Bacteriol. 175:1514-1523(1993).					
RL						
RN	CHARACTERIZATION;					
RX	Medline=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;					
RX	Dionisi H.M., Viale A.M.;					
RT	"Purification and characterization of Chromatium vinosum GroEL and GroES proteins overexpressed in Escherichia coli cells lacking the endogenous groESL operon."					
RT	Protein Expr. Purif. 14:275-282(1998).					
RL	- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress					
CC						
CC						
RESULT 13						
Q6C3F9	PRELIMINARY;	PRT;	457 AA.			
AC	Q6C3F9;					
DT	25-OCT-2004 (TREMBrel. 28, Created)					
DT	25-OCT-2004 (TREMBrel. 28, Last sequence update)					
DE	Similar to sp P08540 Kluyveromyces lactis Potential acid phosphatase.					
DE	ORFname=YALI0E35222g;					
OS	Yarrowia lipolytica CLIB99.					
OC	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.					
NCBI_TaxID	=284591;					
RN	SEQUENCE FROM N.A.					
RP	CHARACTERIZATION;					
RX	Medline=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;					
RX	Dionisi H.M., Viale A.M.;					
RA	Ferreira R., Soncini F., Viale A.M.;					
RT	"Cloning, characterization, and functional expression in Escherichia coli of chaperonin (groESL) genes from the phototrophic sulfur bacterium Chromatium vinosum."					
RT	J. Bacteriol. 175:1514-1523(1993).					
RN	CHARACTERIZATION;					
RX	Medline=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;					
RX	Dionisi H.M., Viale A.M.;					
RA	Fermentation Expr. Purif. 14:275-282(1998).					
RA	- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress					

		A; Note: sequence extracted from NCBI backbone (NCBIN:122968, NCBIPI:126970) C; Superfamily: chaperonin groEL C; Keywords: molecular chaperone
Query Match 91STANKIVWSDPTRLSTFSASLIR-QRVKVQIAELNNVSGQTVSYKRPARKPKBGGAD 67 Best Local Similarity 25.5%; Pred. No. 9.3; Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;	Qy 9 1STANKIVWSDPTRLSTFSASLIR-QRVKVQIAELNNVSGQTVSYKRPARKPKBGGAD 67 Db 82 INRVAASVTFDTIASLNQLTCNLTFGQLEQNYGTTISG-----LPPEKPKNL-- 132	Query Match 3 NKTMOPTSTANKI-VWSDPTRLSTFSASLIRQVKGVLAEIN-----NVS 4 Best Local Similarity 20.7%; Pred. No. 9; Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps
Qy 68 ACVMPNENGSRTVSGSAENLA---TURAEWETHK 101 Db 133 SCIV-NNECKMRCEWDGORETHLETNFURKSEATHK 168	Qy 68 NMGQMVKEYAKTSIDIAQDGTATTYLAQAMVREGLKAVAGMNPMDLKRMNDKVEAA : : Db 128 TEEALKLSKPKCPRMIAQVTISANSDDSIGITIAABAMEKVYGE3VITVECTSLQNL : : Db 106 TLFA5GNAGLGFLLDP 120 Db 188 DVVEGRNOFDRTGLSP 202	Qy 49 GOVSVYKRPAPKPEGCADACVIMPNENGSRTVSGAENL--ATLKAETWETHKRNVD : : Db 128 TEELKLUSKPKCPRMIAQVTISANSDDSIGITIAABAMEKVYGE3VITVECTSLQNL : : Db 145847
RESULT 3		RESULT 5
A75334 [acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - Deinococcus radiodurans C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: A75334 A;Reference number: A75334 A;Status: preliminary A;Molecule type: DNA A;Gene: DR1945 A;Map position: 1 A;Protein family: [acyl-carrier-protein] S-malonyltransferase; [acyl]-carrier-protein] S-mal A;Keywords: acyltransferase; coenzyme A E;7286/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT> F;93/Active site: Ser (covalent substrate-binding) #status predicted R1	Query Match 11.7%; Score 78; DB 2; Length 305; Best Local Similarity 28.9%; Pred. No. 3.1; Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;	Query Match 11.3%; Score 75.5%; DB 2; Length 519; Best Local Similarity 23.4%; Pred. No. 11; Matches 37; Conservative 20; Mismatches 62; Indels 39; Gaps
Qy 13 ANKTKWSDPTRLSTFSASLIR-QRVKVQIAELNNVSGQTVSYKRPARKPKBGG-ADACVI 71 Db 103 AGVLTEDAIRL-TRKRGEMMQAPEGVQMSAIVMD-----PRVVAEVCAQGVV 154	Qy 2 ANKTMOPITSTANKI-VWSDPTRLSTFSASLIRQVKGVLAEIN-----ELNNVSGQ---Y : : Db 370 APRPLQNGSSSSCWPTTAAGEEVCLPSELFLPRASEKGLPKPSGQSPBEW : : Db 52 VSVYKRPAPKPEGCADACVIMPNENGSRTVSGAENL-----ATLKAETWETHKRNVD : : Db 430 CCSLQKQAPAOIQACVCAECLNARAHQSOHTPSGN-----KEWFLYGRVLDRCVCPA : : Db 106 -TLEPSGNAGLGF-----DPTAAIVSSD 128 Db 482 MLSLFVCGTAGIFLMAHYNRVDAIPFPFDPRSYLPPSSD 519	Qy 131 A 131 Db 215 A 215
RESULT 4		RESULT 6
B47073 Chaperonin GroEL - Chromatium vinosum C;Species: Chromatium vinosum C;Accession: B47073 C;Accession: B47073 R;Ferreyn, R. G.; Soncini, F. C.; Viale, A. M. J. Bacteriol. 175, 1514-1523, 1993 A;Title: Cloning, characterization, and functional expression in Escherichia coli of cha A;Reference number: A47073; PMID:9444812 A;Accession: B47073 A;Status: preliminary A;Molecule type: nucleic acid F;93/Active site: 1-56 <FNR> A;Cross-references: UNIPROT:PI1293; GB:M99443; NID:9145007; PIDN:AAA23319.1; PMID:98295987; PMID:9634230 A;Accession: D70972 A;Status: preliminary; nucleic acid sequence not shown; translation not shown;	Query Match 18-Nov-1994 #text_change 09-Jul-2004 Best Local Similarity 20.7%; Pred. No. 9; Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps	Query Match 17-Jul-1998 #text_change 16-Aug-2004 Best Local Similarity 23.4%; Pred. No. 11; Matches 37; Conservative 20; Mismatches 62; Indels 39; Gaps
		C;Species: Mycobacterium tuberculosis (strain H37RV) C;Accession: D70972 R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, J.; Connor, R.; Davies, R.; Rohde, K.; Feil, W. T.; Ghetty, S.; Hamlin, N.; Rajandream, M. A.; Rogers, J.; Rutten, S.; Seeger, K.; Shetton, S.; Squares, R.; A;Authors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. NATURE 393, 537-544, 1998 A;Reference number: A70500; PMID:1070523 A;Accession: D70972 A;Status: preliminary

A; Molecule type: DNA
A; Residues: 1-213 <COL>
A; Cross-references: UNIPROT:050402; GB:AL009198; GB:AL123456; NID:93242262; PIDN:CAA1575
C; Species: *Arabidopsis thaliana*
A; Gene: *ech1*
C; Superfamily: Naphthoate synthase

Query Match 11.0%; Score 73.5; DB 2; Length 213;
Best Local Similarity 27.6%; Pred. No. 5.8; Indels 7; Gaps 3;
Matches 24; Conservative 14; Mismatches 42; DB 2; Length 831;
Query Match 11.0%; Score 73.5; DB 2; Length 831;
Best Local Similarity 25.8%; Pred. No. 30;
Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;
Query Match 11.0%; Score 73.5; DB 2; Length 831;
Best Local Similarity 25.8%; Pred. No. 30;
Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;

Qy 33 LRQPKVGTALLNNVGQVSV----YKRPAKPKPGCADACVIMPENQNSIRTVISSLRQVRVKVIAELNNVSGQ--
Db 1 MRRAAMTQDEASNPCCGDIEAEMCQLMREQOPPAEGVDRVALQRHRNVALTLISHQAA 60
Qy 89 NLATLKAWEWTHKRNVDTLFASGNAGL 115
Db 61 NALNL-ASWRRLKLRLDDL--AGESQL 84

RESULT 7
T51668 myb-related transcription factor MYB61 [imported] - *Arabidopsis thaliana* (fragment)
C; Species: *Arabidopsis thaliana* (mouse-ear cress)
C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C; Accession: T51668
R; Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J.
R; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A; Title: Towards functional characterisation of the members of the R2R3-MYB gene from Arabidopsis
A; Reference number: 214349; PMID:9839469
A; Accession: T51668
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-291 <KRA>
A; Cross-references: UNIPROT:Q9SBF9; EMBL:AF062896; PIDN: AAC83618.1
A; Experimental source: cultivar Columbia
C; Genetics:
A; Gene: MYB61
A; Map position: I
C; Keywords: transcription factor

Query Match 11.0%; Score 73.5; DB 2; Length 291;
Best Local Similarity 21.9%; Pred. No. 8.5; Indels 19; Gaps 4;
Matches 30; Conservative 21; Mismatches 67; DB 2; Length 291;
Query Match 11.0%; Score 73.5; DB 2; Length 291;
Best Local Similarity 21.9%; Pred. No. 8.5; Indels 19; Gaps 4;

Qy 3 NKTQPISTSANKIIVWSDDPTRLSTFSALLRQVRVKVIAELNNVVS-----GOX 51
Db 78 HKSPSSSATNQDFFLERPSDLSDYGFQKLNFNSNLGSVTDSSLCSMIPQQPSQNM 137
Qy 52 V-SVYKRPAPKPKPGCADACVIMPENQNSIRTVISSLRQVRVKVIAELNNVVS-----GOX 110
Db 138 VGSTLQTPV-----CVRSISLSDHNNSSSP1GQDGHVTKLAAPNWFQNNNTSNFF- 190
Qy 111 GNAGLGFLDPTAAVSS 127
Db 191 DNGGFSWSTPNSSSTSS 2 07

RESULT 8
A11515 ORFA of *Listeria seeligeri*, (LpxTG motif) homolog lin0665 [imported] - *Listeria innocua*
C; Species: *Listeria innocua*
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: A11515
R; Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Durand, L.; Dussurge, O.; Entian, K.D.; Faihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierre, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, C; Title: Comparative genomics of *Listeria* species.
A; Reference number: AB1077; PMID:21537279; PMID:11679669

Qy 12 TANKIVSDDPTRLSTFSALLRQVRVKVIAELNNVSGQVYKRPARK-----PEGC 65
Db 191 TNNETLNDPLVIG-----NKPRPLSESEYDAFTASFVNMKEVPKAIIHWEDFGR 242
Qy 66 ADACVIMPENQNSIRTV-----AEYLTLKAWEWTHKRNVDTLFASGNAGLGP 117
Db 243 ANASRLHNYRKICTFDDIQGTGAWVVAVATIQVSRIPULSEQKIIIFGAGTAGIGI 302
Qy 118 LDPTAAVSSDT 129
Db 303 ADQLSAQLMRET 314

RESULT 10
B64446 Formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - Methanococcus jannaschii
C; Species: *Methanococcus jannaschii*
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

C;Accession: B64446
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.; Reich, C.I.; Overbeek, R.; Kirnness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodkik, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 C;Accession: T14951
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.;Reference number: A64300; PMID:96337999; PMID:8688087
 A;Cross-references: UNIPROT:Q58571; BUL>
 A;Residues: 1-273
 A;Molecule type: DNA
 C;Genetics:
 A;Map position: FOR110572-1111393
 C;Superfamily: Formylmethanofuran dehydrogenase, subunit C
 C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten
 Query Match Score 72; DB 2; Length 273;
 Best Local Similarity 27.6%; Pred. No. 11; Mismatches 31; Indels 26; Gaps 4;
 Matches 27; Conservative 14; Mismatches 31; Indels 26; Gaps 4;
 Qy 34 RQRVKG--IAELINNSGQYVSYKRPAPK-----PEGGADACVIMPNEN 76
 Db 43 RKRKVADDFDVELNDIEGEPRIVKNSSPKLKYIGSKMTKGEIVVEG--DAGMYVGAEW 100
 Qy 77 QSIRTVISGSAENTLAKAEWETHKRNTVDTLFASGNAG 114
 Db 101 KGGKIVVNGNAES-----WAGONMKGGELLIGKGNAG 131
 RESULT 11
 T11951
 hypothetical protein Y035 - *Yersinia pestis* plasmid pMT1.
 C;Species: *Yersinia pestis*
 C;Date: 20-Sep-1999 #text_change 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T14951
 R;Lindler, L.B.; Piano, G.V.; Burland, V.; Mayhew, G.P.; Blattner, F.R.
 Infect. Immun. 66, 5731-5742; 1998
 A;Title: Complete DNA sequence and detailed analysis of the *Yersinia pestis* KIM5 plasmid
 A;Reference number: Z18268; MUID:99043898; PMID:9826348
 A;Accession: T14951
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-220 <LINK>
 C;Cross-references: UNIPROT:O68736; EMBL:A074611; NID:93883035; PIDN:AA88
 C;Genetics:
 A;Gene: Y1035
 Query Match Score 10.7%; DB 2; Length 220;
 Best Local Similarity 20.1%; Pred. No. 9..6;
 Matches 29; Conservative 28; Mismatches 66; Indels 21; Gaps 6;
 Qy 1 MANKTMQ----PITSTANKIWW-SDPTPLSITFSASLUR---QRVKGIAELINNNVSGQ 50
 Db 65 LVGKTVQLSAGITNSKSASDFTWTSNDNDEVATSGTGLTVGTVQKTVTATDKQTQTLSA 124
 Qy 51 YVSIVKRPAPKPEGGADACVIMPN----ENQSIIRTIVISGSAENLATKAEGWETHKRNTD 105
 Db 125 SVEITVKPV----SVESTVTPDSTSVEKGKSVKLRLVYQPSNATNKKVWTISKNSOKA 179
 Qy 106 TLFASGN-AGLGFIDPAAIVSSD 128
 Db 180 TVDQNGNVAVGAVGTATIEVVSQD 203
 RESULT 12
 T1Q1674
 protein kinase TMK1 (EC 2.7.1.-), receptor type precursor - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse ear cress)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: T1Q1674
 A;Cross-references: UNIPROT:P43298; GB:L00670; NID:9166887; PIDN:AAA32876.1; PMID:13332795
 A;Status: preliminary; protein kinase X221; leucine-rich alpha-2-glycoprotein repeat homology; phosphotransferase; receptor; serine/threonine kinase; CHA>
 A;Residues: 1-942 <CHAs>
 A;Cross-references: UNIPROT:P43298; GB:L00670; NID:9166887; PIDN:AAA32876.1; PMID:13332795
 A;Keywords: ARP; autophosphorylation; glycoprotein; phosphotransferase; receptor; serine/threonine kinase; X221; leucine-rich alpha-2-glycoprotein repeat homology; phosphotransferase; receptor; serine/threonine kinase; CHA>
 A;Molecule type: DNA
 A;Accession: JQ1674
 C;Accession: F1-12/11/Domain: signal sequence #status predicted <SIG>
 F:1-12/11/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:12/12-13/15/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:13/16-16/18/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:16/17-18/18/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:18/17-20/9/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:21/0-23/22/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:23-25/25/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:25/26-27/9/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:28/0-28/9/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:29/0-30/11/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:32/4-34/6/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:36/3-36/6/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:38/7-41/0/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:41/1-43/4/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:48/0-50/3/Domain: transmembrane #status predicted <TMM>
 F:50/6-87/2/Domain: protein kinase homology <KIN>
 F:59/4-60/2/Region: protein kinase ATP-binding motif
 F:56/99-158/164/171/363/533/587/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:61/6, 63/4, 71/7, 71/9/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match Score 10.7%; DB 1; Length 942;
 Best Local Similarity 23.6%; Pred. No. 56; Mismatches 26; Gaps 11; Matches 38; Conservative 26; Mismatches 38; Indels 59; Gaps 11;

Qy 4 KTMOPITSTANKIWWSDP----TRLSTTFPSASLLQRQVKGV----IAEL 44
 Db 37 KSLNPNSPSFG----WSDDPCKWTHIVCTGTKEV-TRIQIGHSGLQQTLSPLRNLSEL 90
 Qy 45 -----NNVSGQYVSYKRPARKPEGGADACVIMPNQNQSTRTVSGSAENLATLKA-- 95
 Db 91 ERLEQWNNSIG-----PVPSLGLASLQVLMMS-MNNFDPSIPSDVFGQLTLSQSYV 141
 Qy 96 -----EWEETHK--PRVYDTL--FASGNAGL----GPFLDP 120
 Db 142 IDNNPFKSWBIPESLRNALQNFANSANVGSLSLQPGFLGP 182

RESULT 13
 S38149
 S38149 protein - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein YKR072C
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C;Accession: S38149; S54982; S43078
 R;Pohl, T.M.; Pohl, F.M.
 submitted to the Protein Sequence Database, March 1994
 A;Reference number: S37897
 A;Accession: S38149
 A;Molecule type: DNA
 A;Residues: 1-562 <POH>
 A;Cross-references: UNIPROT:P36024; EMBL:228297; NID:9486544; PMID:9486545; MIPS:YKR072C
 A;Experimental source: Strain S288C
 R;di Cono, C.J.; Boe, R.; Arndt, K.T.
 Genetics 139, 95-107, 1995
 A;Title: Overexpression of SIS2, which contains an extremely acidic region, increases the
 A;Reference number: S54982; MUID:95220693; PMID:705654
 A;Cross-references: EMBL:U01878; NID:9430983; PIDN:AAA80000.1; PMID:9430984

C;Genetics:
A;Gene: SGD:SIS2
A;Cross-references: SGD:S0001780; MIPS:YKR072C
A;Map Position: 11R
C;Keywords: nucleus

Query Match 10.7%; Score 71; DB 2; Length 562;
Best Local Similarity 23.7%; Pred. No. 34;
Matches 27; Conservative 23; Mismatches 52; Indels 12; Gaps 4;

Qy 4 KTMQPITSTANKIWIWNSDPL--TRLSTTFSASLRLQRVKVGTABLNNVSGQTVSVYKRPA 59
Db 68 KSMNNTGTSGAVSNTBPGKLKRVPAVTFSDIKQQQDQSLTQLNDERTSPNSNPA 127

Qy 60 PKPEGCADACVIMPENOSITY-IGSAENNLATLKAWEHTKRN---VDTL 107
Db 128 PYNSNTPGNHNAVPNHTNTSRTQLSGSP-LVNEMKDYPKKDLSALKIVDTM 179

RESULT 14

A;Residues: 1-536 <ZUB>
A;Cross-references: UNIPROT:P23447; GB:MF4965
R;Albertini, A.M.; Caranori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J; Bacteriol. 173, 3573-3579, 1991
A;Title: The fla locus of *Bacillus subtilis* is part of a large operon coding for flagellin
A;Reference number: A42365; PMID:91258343; MUID:1828465
A;Accession: A42365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 355-536 <ALB>
A;Cross-references: GB:MT2716; EMBL:X59904; PIDN:CAA39520_1; PID:93979709
R;Kunst, F.; Ogasawa, N.; Moszer, I.; Albertini, A.M.; Altoni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brondum, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.; Nature 390, 249-256, 1997
A;Authors: Foulonger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleni, J.; Harzappel, S.; Hildebrand, H.; Holzapfel, S.; Huilo, M.P.R.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurata, K.; Lardinois, A.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Ogawa, K.; Ogiwara, H.; Oneda, Y.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Schleich, S.; Schreeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, Akeuchi, M.; Tamakoshi, A.; Teraiwa, T.; Terpstra, P.; Togomi, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; PMID:38044033; MUID:9384377
A;Accession: B69524
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-536 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; PID:92633902; PIDN:CAB13494_1; PID:e1185212;
A;Experimental source: strain 168
C;Genetics:
A;Gene: filF

Query Match 10.6%; Score 70.5%; DB 2; Length 536;
Best Local Similarity 25.8%; Pred. No. 36;
Matches 33; Conservative 19; Mismatches 57; Indels 19; Gaps 4;

Qy 1 MANKTMQPITSTANKIWIWNSDPL--TRLSTTFSASLRLQRVKVGT---AEILNNVSGQTVSVY 55
Db 8 MKNKSE-----FWRKRSKQLQKILMSALAALIIIGLIISVFAINSKMAPLYKDLS 58

Qy 56 KRPAPKPEGGDADCYMPENOSITY-IGSAENNLATLKAWEHTKRN---AEWETHKRNVDTLPASG 111
Db 59 AEEAGGIKEELDAKKW-PNELSNGGTIVSPEQDVNLKVQMAAEGLPKTGSDIDSFGQ 117

Qy 112 NAGLGFID 119
Db 118 NAGGFGLTD 125

Search completed: June 1, 2005, 09:46:48
Job time : 25 secs

C;Genetics:
A;Gene: SGD:SIS2
A;Cross-references: SGD:S0001780; MIPS:YKR072C
A;Map Position: 11R
C;Keywords: nucleus

Query Match 10.6%; Score 70.5%; DB 2; Length 414;
Best Local Similarity 21.9%; Pred. No. 26;
Matches 30; Conservative 20; Mismatches 68; Indels 19; Gaps 4;

Qy 3 NKTMQPITSTANKIWIWNSDPL--TRLSTTFSASLRLQRVKVGTABLNNV---GTY 51
Db 153 HKSPSSSSATQNDDFFLERPSLSDYFGQKLNFSNLGSVTTDSLCSMIPPOFSPGNM 212

Qy 52 V-SVYKRPAPKPEGGDADCYMPENOSITY-IGSAENNLATLKAWEHTKRN---GTY 51
Db 213 CVKPSISSLQTPV----CVKPSISSLPDNNNSSPISCGDHYKLAAPNWEFOTNNTNTSNNF - 265

Qy 111 GNAGLGFLDPAIAVSS 127
Db 266 DNGGFSMSIPNSSTSSS 282

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OM protein - protein search, using SW model.

Run on: June 1, 2005, 09:38:08 ; search time 91 Seconds (without alignments)

Scoring table: BLOSUM62 Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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18: /cgn2_6/ptodata/1/pubcaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubcaa/US60_PUB.pep:*

20: /cgn2_6/ptodata/1/pubcaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	666	100.0	131	14	US-10-243-739-81	Sequence 81, Appl
2	666	100.0	131	14	US-10-244-065-81	Sequence 81, Appl
3	666	100.0	131	14	US-10-288-454-81	Sequence 81, Appl
4	666	100.0	131	15	US-10-344-190-96	Sequence 96, Appl
5	666	100.0	131	15	US-10-468-811-93	Sequence 93, Appl
6	666	100.0	131	15	US-10-288-456-113	Sequence 113, Appl
7	666	100.0	131	15	US-10-622-064-18	Sequence 18, Appl
8	666	100.0	131	15	US-10-617-876-3	Sequence 3, Appl
9	666	100.0	131	15	US-10-622-124-29	Sequence 29, Appl
10	666	100.0	131	16	US-10-622-087-29	Sequence 29, Appl
11	660	99.1	131	14	US-10-243-739-80	Sequence 80, Appl
12	660	99.1	131	14	US-10-244-065-80	Sequence 80, Appl
13	660	99.1	131	14	US-10-289-454-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1 US-10-243-739-81 ; Publication US/10243739 ; Publication No. US20030091593A1 ; GENERAL INFORMATION: ; APPLICANT: Bachmann, Martin F. ; APPLICANT: Storni, Tazio ; APPLICANT: Lechner, Franziska ; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of Immune Responses Induced by Virus Like Particles ; FILE REFERENCE: 1700_0210.01 ; CURRENT APPLICATION NUMBER: US/10/243,739 ; CURRENT FILING DATE: 2002-09-16 ; PRIOR APPLICATION NUMBER: 60/318,967 ; PRIOR FILING DATE: 2001-09-14 ; NUMBER OF SEQ ID NOS: 73 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 81 ; LENGTH: 131 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: AP205 coat protein

US-10-243-739-81

Query Match Best Local Similarity 100.0% ; Pred. No. 3,6e-71; Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKTMQPTSTANKIVWDPTPLSTTSASLRLQRVKGIAELNNVSCQYVSVKRKAP 60 Db 1 MANKTMQPTSTANKIVWDPTPLSTTSASLRLQRVKGIAELNNVSCQYVSVKRKAP 60

Qy 61 KPEGCADACVIMPNEQNSRTVSGSAENLATLKAENETHKRNDTTLFASGNAGLGFLLP 120 Db 61 KPEGCADACVIMPNEQNSRTVSGSAENLATLKAENETHKRNDTTLFASGNAGLGFLLP 120

Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131

RESULT 2
 US-10-244-065-81
 ; Sequence 81, Application US/102444065
 ; Publication No. US20030099668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin P.
 ; APPLICANT: Storni, Tazio
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Tisot, Alain
 ; APPLICANT: Schwarz, Katrin
 ; APPLICANT: Meijerink, Edwin
 ; APPLICANT: Lipowsky, Gerad
 ; APPLICANT: Pumpens, Paul
 ; APPLICANT: Cielens, Indulis
 ; APPLICANT: Renhoffa, Regina
 ; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
 ; TITLE OF INVENTION: Method of Preparation and Use
 ; FILE REFERENCE: 1700_0220001
 ; CURRENT APPLICATION NUMBER: US/10/244,065
 ; PRIOR FILING DATE: 2002-09-16
 ; CURRENT FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: 60/318,994
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 81
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: AP205 coat protein
 US-10-244-065-81

Query Match 100.0%; Score 666; DB 14; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.6e-71;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKTQPITSTANKIVWSDPTRLSTTFASLLRQRVKVIAELNNVSSQQYVSYKRPAP 60
 Db 1 MANKTQPITSTANKIVWSDPTRLSTTFASLLRQRVKVIAELNNVSSQQYVSYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSRTVTSGSAENLATKAEMETHKRNDTLFASGNAGLGFDP 120
 Db 61 KPEGCADACVIMPNENQSRTVTSGSAENLATKAEMETHKRNDTLFASGNAGLGFDP 120

Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131

RESULT 4
 US-10-346-190-96
 ; Sequence 96, Application US/10346190
 ; Publication No. US20030219459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Peilicoli, Erica
 ; APPLICANT: Reuner, Wolfgang A.
 ; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
 ; FILE REFERENCE: 1700_0298003
 ; CURRENT APPLICATION NUMBER: US/10/346,190
 ; CURRENT FILING DATE: 2003-01-17
 ; PRIOR APPLICATION NUMBER: 60/396,550
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/393,725
 ; PRIOR FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: 10/050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; NUMBER OF SEQ ID NOS: 164
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 96
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: RNA-phage AP205
 US-10-346-190-96

Query Match 100.0%; Score 666; DB 15; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.6e-71;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKTQPITSTANKIVWSDPTRLSTTFASLLRQRVKVIAELNNVSSQQYVSYKRPAP 60
 Db 1 MANKTQPITSTANKIVWSDPTRLSTTFASLLRQRVKVIAELNNVSSQQYVSYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSRTVTSGSAENLATKAEMETHKRNDTLFASGNAGLGFDP 120
 Db 61 KPEGCADACVIMPNENQSRTVTSGSAENLATKAEMETHKRNDTLFASGNAGLGFDP 120

FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-289-456-113

RESULT 5

Qy 121 TAAIVSSDTA 131
Db 121 TAAIVSSDTA 131

Sequence 93, Application US/10465811
Publication No. US201004005338A1
GENERAL INFORMATION:
APPLICANT: BACHMANN, MARTIN F
APPLICANT: RENNER, WOLFGANG A
TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS
TITLE OF INVENTION: METHOD OF PREPARATION AND USE
FILE REFERENCE: 1700.023004
CURRENT APPLICATION NUMBER: US/10/465,811
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 60/389,898
PRIOR FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 131
SEQ ID NO 93
LENGTH: 131
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage AP205 mutant
US-10-465-811-93

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3. 6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKTMQPTSTANKIWSDPTRLSTFSASLIRQRYKVGIAELNNVSGQYVSKRPP 60
Db 1 MANKTMQPTSTANKIWSDPTRLSTFSASLIRQRYKVGIAELNNVSGQYVSKRPP 60

Qy 61 KPEGCADACVIMPNENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGLDP 120
Db 61 KPEGCADACVIMPNENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGLDP 120

RESULT 7

US-10-622-064-18

Sequence 18, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrik F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
PRIORITY FILING DATE: 2003-07-18
PRIORITY APPLICATION NUMBER: US 60/396,575
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 131
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Bacteriophage APP205 mutant
US-10-622-064-18

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3. 6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKTMQPTSTANKIWSDPTRLSTFSASLIRQRYKVGIAELNNVSGQYVSKRPP 60
Db 1 MANKTMQPTSTANKIWSDPTRLSTFSASLIRQRYKVGIAELNNVSGQYVSKRPP 60

Qy 61 KPEGCADACVIMPNENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGLDP 120
Db 61 KPEGCADACVIMPNENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGLDP 120

RESULT 8

US-10-617-876-3

Sequence 3, Application US/10617876
Publication No. US20040076611A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrik F
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 113
LENGTH: 131
TYPE: PRT
ORGANISM: Artificial Sequence
TITLE OF INVENTION: Molecular Antigen Arrays
FILE REFERENCE: 1700.0310001

CURRENT APPLICATION NUMBER: US/10/617,876
 CURRENT FILING DATE: 2003-07-14
 PRIORITY NUMBER: US 60/396,126
 PRIORITY FILING DATE: 2002-07-17
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 131
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Bacteriophage AP205 mutant
 US-10-617-876-3

Query Match 100.0%; Score 666; DB 15; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.6e-71;
 Matches 131; Conservative 0; Indels 0; Gaps 0;

Qy 1 MANKTMQPTSTANKIVWSDPTRLSTTFASLLRQRVKGIAELNNVSGQQVSVYKRPAP 60
 Db 1 MANKTMQPTSTANKIVWSDPTRLSTTFASLLRQRVKGIAELNNVSGQQVSVYKRPAP 60

Qy 61 KPEGGADAVIMPENQSLRTVISSAENLATKAWEETHKRNVDTLFFASGNAGLGFDP 120
 Db 61 KPEGGADAVIMPENQSLRTVISSAENLATKAWEETHKRNVDTLFFASGNAGLGFDP 120

Qy 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 9
 US-10-622-124-29
 Sequence 29 Application US/10322124
 Publication No. US20040076645A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin F.
 ALTERNATIVE APPLICANT: Almala, Tuuli
 TITLE OF INVENTION: Ghrelin-Carrier Conjugates
 FILE REFERENCE: 1700_0340001
 CURRENT APPLICATION NUMBER: US/10/622,124
 CURRENT FILING DATE: 2003-07-18
 PRIOR APPLICATION NUMBER: US 60/396,638
 PRIOR FILING DATE: 2003-07-19
 NUMBER OF SEQ ID NOS: 146
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 29
 LENGTH: 131
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: AP205 coat protein
 US-10-622-124-29

Query Match 100.0%; Score 666; DB 15; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.6e-71;
 Matches 131; Conservative 0; Indels 0; Gaps 0;

Qy 1 MANKTMQPTSTANKIVWSDPTRLSTTFASLLRQRVKGIAELNNVSGQQVSVYKRPAP 60
 Db 1 MANKTMQPTSTANKIVWSDPTRLSTTFASLLRQRVKGIAELNNVSGQQVSVYKRPAP 60

Qy 61 KPEGGADAVIMPENQSLRTVISSAENLATKAWEETHKRNVDTLFFASGNAGLGFDP 120
 Db 61 KPEGGADAVIMPENQSLRTVISSAENLATKAWEETHKRNVDTLFFASGNAGLGFDP 120

Qy 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 11
 US-10-243-739-80
 Sequence 80 Application US/10243739
 Publication No. US2003009159A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin F.
 ALTERNATIVE APPLICANT: Stormi, Tazio
 TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of Immune Responses Induced by Virus Like Particles
 FILE REFERENCE: 1700_0210001
 CURRENT APPLICATION NUMBER: US/10/243,739
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/318,967
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 80
 LENGTH: 131
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: AP205 coat protein
 US-10-243-739-80

Query Match 99.1%; Score 660; DB 14; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 130; Conservative 0; Indels 1; Gaps 0;

RESULT 10
 US-10-622-087-29

FILE REFERENCE: 1700_0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIORITY APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIORITY APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIORITY APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIORITY APPLICATION NUMBER: US 60/331,045
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 80
LENGTH: 131
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Ap205 coat protein
US-10-289-454-80

Query Match 99.1%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 1..9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTMOPITSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60
Db 1 MANKPMQPTSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60

Query Match 99.1%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 1..9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTMOPITSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60
Db 1 MANKPMQPTSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60

RESULT 14
US-10-346-190-95
Sequence 95, Application US/10346190
Publication No. US2003019459A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhoffs, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method Of Preparation and Use
FILE REFERENCE: 1700_0360001
CURRENT APPLICATION NUMBER: US/10/244,065
CURRENT FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/318,994
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 80
LENGTH: 131
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: AP205 coat protein
US-10-244-065-80

Query Match 99.1%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 1..9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTMOPITSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60
Db 1 MANKPMQPTSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60

Query Match 99.1%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 1..9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTMOPITSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60
Db 1 MANKPMQPTSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60

Query Match 99.1%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 1..9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTMOPITSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60
Db 1 MANKPMQPTSTANKIVWSDPTRLSTIFSASLRLQRVKVIAELNNVSGQYVSYKRPA P 60

RESULT 13
US-10-289-454-80
Sequence 80, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases

Qy 1 MANKTMQPTISTANKIIVNSDPTRSLSTFASILLRQRYKGIAELANNVSGQQYVSYYKRPA P 60
 Db 1 MANKEMQPTISTANKIIVNSDPTRSLSTFASILLRQRYKGIAELANNVSGQQYVSYYKRPA P 60
 Qy 61 KPEGCADAYCIMPNENQSRTVISSAENLATLKAEWETHKRNDTILPASGNAGLGFLDP 120
 Db 61 KPEGCADAYCIMPNENQSRTVISSAENLATLKAEWETHKRNDTILPASGNAGLGFLDP 120
 Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131

RESULT 15
 US-10-465-811-90
 Sequence 90, Application US/10465811
 Publication No. US20040005338A1
 GENERAL INFORMATION:
 APPLICANT: BACHMANN, MARTIN F.
 ATTORNEY: RENNER, WOLFGANG A.
 TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
 TITLE OF INVENTION: METHOD OF PREPARATION AND USE
 FILE REFERENCE: 1700_0290004
 CURRENT APPLICATION NUMBER: US/10/465,811
 CURRENT FILING DATE: 2003-06-20
 PRIOR APPLICATION NUMBER: US 60/389,898
 PRIOR FILING DATE: 2002-06-20
 NUMBER OF SEQ ID NOS: 131
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 90
 LENGTH: 131
 TYPE: PRT
 ORGANISM: Bacteriophage AP205
 US-10-465-811-90

Query Match 99.1%; Score 660; DB 15; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTMQPTISTANKIIVNSDPTRSLSTFASILLRQRYKGIAELANNVSGQQYVSYYKRPA P 60
 Db 1 MANKEMQPTISTANKIIVNSDPTRSLSTFASILLRQRYKGIAELANNVSGQQYVSYYKRPA P 60
 Qy 61 KPEGCADAYCIMPNENQSRTVISSAENLATLKAEWETHKRNDTILPASGNAGLGFLDP 120
 Db 61 KPEGCADAYCIMPNENQSRTVISSAENLATLKAEWETHKRNDTILPASGNAGLGFLDP 120
 Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131

Search completed: June 1, 2005, 09:51:00
 Job time : 92 secs

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Om protein - protein search, using sw model

Run on: June 1, 2005, 09:35:42 ; Search time 30 Seconds
 (without alignments)
 325.968 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANTMQPITSTANKIVNSD.....NAGTGFIDPTAAIVSDDTA 131

Scoring table: BL0SNM62

Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgm2_6/pctodata/1/iaa/5A_COMB.pep:
 2: /cgm2_6/pctodata/1/iaa/5B_COMB.pep:
 3: /cgm2_6/pctodata/1/iaa/6A_COMB.pep:
 4: /cgm2_6/pctodata/1/iaa/6B_COMB.pep:
 5: /cgm2_6/pctodata/1/iaa/PICTUS_COMB.pep:
 6: /cgm2_6/pctodata/1/iaa/backfile1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	79	11.9	312	4	US-09-313-942-10	Sequence 10, Appli
2	79	11.9	488	2	US-08-599-455B-5	Sequence 5, Appli
3	79	11.9	488	3	US-09-069-781B-5	Sequence 5, Appli
4	79	11.9	488	3	US-09-137-132-5	Sequence 5, Appli
5	79	11.9	488	3	US-08-864-564A-5	Sequence 5, Appli
6	79	11.9	488	4	US-09-094-410-5	Sequence 5, Appli
7	79	11.9	488	4	US-08-708-123D-5	Sequence 5, Appli
8	79	11.9	488	4	US-08-583-153A-5	Sequence 5, Appli
9	79	11.9	488	2	US-08-638-524B-5	Sequence 4, Appli
10	79	11.9	658	2	US-08-825-558-4	Sequence 4, Appli
11	79	11.9	658	3	US-09-312-611-4	Sequence 4, Appli
12	79	11.9	708	1	US-07-797-556-2	Sequence 2, Appli
13	79	11.9	708	1	US-08-308-881-2	Sequence 2, Appli
14	79	11.9	708	2	US-09-058-263-2	Sequence 2, Appli
15	79	11.9	708	3	US-09-058-264-2	Sequence 2, Appli
16	79	11.9	708	4	US-09-455-962-2	Sequence 2, Appli
17	79	11.9	708	5	PCT-US95-06530-2	Sequence 7, Appli
18	79	11.9	859	4	US-09-313-942-7	Sequence 6, Appli
19	79	11.9	918	2	US-08-825-558-6	Sequence 6, Appli
20	79	11.9	918	3	US-09-312-611-6	Sequence 3, Appli
21	79	11.9	918	4	US-09-853-180B-3	Sequence 9, Appli
22	79	11.9	951	4	US-09-313-942-9	Sequence 2, Appli
23	79	11.9	1158	4	US-09-313-942-26	Sequence 26, Appli
24	79	11.9	1168	4	US-09-313-942-24	Sequence 24, Appli
25	73	11.0	488	4	US-09-252-991A-285B5	Sequence 28535, Appli
26	73	11.0	185	4	US-09-252-991A-31599	Sequence 31599, Appli

ALIGNMENTS

RESULT 1
 US-09-313-942-10
 ; Sequence 10, Application US/09313942
 ; Patent No. 6472179

; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT APPLICATION NUMBER: US/09/313,942
 ; CURRENT FILING DATE: 1999-05-19
 ; PRIORITY APPLICATION NUMBER: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIORITY APPLICATION NUMBER: 60/101,858
 ; PRIORITY FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSBQ for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-313-942-10

Query Match Similarity 11.9%; Score 79; DB 4; Length 332;
 Best Local Similarity 25.5%; Pred. No. 0.35; Matches 25; Conservatve 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWSDPTRISTFESASLIR-QRVKVQGIAELNNVSGQYVSYYKRPAPKGAD 67
 Db 82 INRTASSVFTDIALNQLTCNLTFQLEQVYGITLISG-----LPPEPKRNLI-- 132

Qy 68 ACVIMPNNQSTRVTSSAENA---TLKAEWEHTK 101
 Db 133 SCIV--NEGKKNRCEWDGGRETHLETFLKSEWATHK 168

RESLT 2
 US-08-599-455B-5
 ; Sequence 5, Application US/08599455B
 ; Patent No. 597621

; GENERAL INFORMATION:
 ; APPLICANT: Tarcaglia, Louis A.
 ; APPLICANT: Tepper, Robert I.
 ; APPLICANT: Culipper, Janice A.
 ; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE BODY WEIGHT USING THE OB RECEPTOR
 ; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street

Result No.	Score	Query	Match	Length	DB ID	Description
1	79	11.9	312	4	US-09-313-942-10	Sequence 10, Appli
2	79	11.9	488	2	US-08-599-455B-5	Sequence 5, Appli
3	79	11.9	488	3	US-09-069-781B-5	Sequence 5, Appli
4	79	11.9	488	3	US-09-137-132-5	Sequence 5, Appli
5	79	11.9	488	3	US-08-864-564A-5	Sequence 5, Appli
6	79	11.9	488	4	US-09-094-410-5	Sequence 5, Appli
7	79	11.9	488	4	US-08-708-123D-5	Sequence 5, Appli
8	79	11.9	488	4	US-08-583-153A-5	Sequence 5, Appli
9	79	11.9	488	2	US-08-638-524B-5	Sequence 4, Appli
10	79	11.9	658	2	US-08-825-558-4	Sequence 4, Appli
11	79	11.9	658	3	US-09-312-611-4	Sequence 4, Appli
12	79	11.9	708	1	US-07-797-556-2	Sequence 2, Appli
13	79	11.9	708	1	US-08-308-881-2	Sequence 2, Appli
14	79	11.9	708	2	US-09-058-263-2	Sequence 2, Appli
15	79	11.9	708	3	US-09-058-264-2	Sequence 2, Appli
16	79	11.9	708	4	US-09-455-962-2	Sequence 2, Appli
17	79	11.9	708	5	PCT-US95-06530-2	Sequence 7, Appli
18	79	11.9	859	4	US-09-313-942-7	Sequence 6, Appli
19	79	11.9	918	2	US-08-825-558-6	Sequence 6, Appli
20	79	11.9	918	3	US-09-312-611-6	Sequence 3, Appli
21	79	11.9	918	4	US-09-853-180B-3	Sequence 9, Appli
22	79	11.9	951	4	US-09-313-942-9	Sequence 2, Appli
23	79	11.9	1158	4	US-09-313-942-26	Sequence 26, Appli
24	79	11.9	1168	4	US-09-313-942-24	Sequence 24, Appli
25	73	11.0	488	4	US-09-252-991A-285B5	Sequence 28535, Appli
26	73	11.0	185	4	US-09-252-991A-31599	Sequence 31599, Appli

CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/599,455B
 FILING DATE: 22-JAN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/017001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-9906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 -08-599-455B-5

Query Match 11.9%; Score 79; DB 2; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0 62; Indels 16; Gaps 5;
 Matches 25; Conservative 21; Mismatches 36; Delins 16; Gaps 5;

9	ITSTANKIIVWSDPTRLSTTSASLLR-QRVKGIAELNNVSGQQYVSYKRPAPKPEGCAD 67
53	INTTASSVFTDIASLNQLTQNLTPGQLEQNYGITISG-----LPPEPKPNL-- 103
68	ACVIMENENQSIIRTIVSGAENLA---TLKAEWETHK 101
104	SCIV--NEGKKNRCEWDGGRETHLETNTLKSSEWATHK 139

SUL3
 -09-069-781B-5
 Sequence 5, Application US/09069781B
 Patent No. 6287782
 GENERAL INFORMATION:
 APPLICANT: Tarraglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/069,781B
 FILING DATE: 29-APR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,564
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: US/08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: US/08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: US/08/539,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: US/08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: US/08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: US/08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: US/08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: US/08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/082001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-069-781B-5

Query Match 11.9%; Score 79; DB 3; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0 62; Indels 36; Mismatches 21; Gaps 5;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy	9 ITSTANKIIVWSDPTRLSTTSASLLR-QRVKGIAELNNVSGQQYVSYKRPAPKPEGCAD 67
Db	53 INTTASSVFTDIASLNQLTQNLTPGQLEQNYGITISG-----LPPEPKPNL-- 103
Qy	68 ACVIMENENQSIIRTIVSGAENLA---TLKAEWETHK 101
Db	104 SCIV--NEGKKNRCEWDGGRETHLETNTLKSSEWATHK 139

RESULT 4
 US-09-137-132-5
 Sequence 5, Application US/09137132
 ; Sequence 5, Application US/09137132
 ; Patent No. 6380363
 ; GENERAL INFORMATION:
 ; APPLICANT: Tarraglia, Louis A.
 ; APPLICANT: Tepper, Robert I.
 ; APPLICANT: Culpepper, Janice A.
 ; APPLICANT: White, David W.
 ; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 ; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 ; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02110-2804

COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/137,132
 FILING DATE: 18-AUG-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/864,564
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: 08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: 08/763,8,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/552,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/019004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-137-132-5

Query Match 11.9%; Score 79; DB 3; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0.62; Indels 16; Gaps 5;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWSDPTRLSITFSASLRL-QRVKVIGIAELNNVSGQYVSYKRPAPKPEGGAD 67
 Db 53 INRTASSVFTDITASLNQILTQCNILTFQLEQVYGTITISG-----LPPEPKPNL-- 103

Qy 68 ACVIMPNENQSIIRTVISSAENLA---TLLKAEMETH 101
 Db 104 SCIV--NEGKKMRCEWDGGRETHLETNTLKSEWATHK 139

RESULT 5
 US-08-864-564A-5
 Sequence 5, Application US/08864564A
 Patent No. 6395498
 GENERAL INFORMATION:
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.

RESULT 6
 US-09-094-410-5
 Sequence 5, Application US/09094410
 Patent No. 6403552
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,410
FILING DATE: 09-JUN-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/854,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/559,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/559,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/556,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-094-410-5

Query Match 11.9%; Score 79; DB 4; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62; Gaps 5;
Matches 25; Conservative 21; Nismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVWSDPTRSLTFSASLIR-ORVKVGIAELNNVSGOVSYKRPAPKEGGAD 67
Db 53 INRTASSVFTDIALNLTQTCNLTFQOLEQNYGITISG-----LPPEPKPNL-- 103

Qy 68 ACVIMPNENOSIRTIVSGAENLA---TLKAEMETHK 101
Db 104 SCIV--NEGRKMRCEWDGGRETHLETNTFLKSEWATHK 139

RESULT 8
US-08-583-153A-5
Sequence 5, Application US/08583153A
Patent No. 6506877
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPARTENT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 41

RESULT 7
US-08-708-123D-5
Sequence 5, Application US/08708123D
Patent No. 6482927
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPARTENT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPARTENT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 41

TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
APPLICATION NUMBER: 03-SEP-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/638,524
APPLICATION NUMBER: 26-APR-1996
APPLICATION NUMBER: 08/599,455
APPLICATION NUMBER: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
APPLICATION NUMBER: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
APPLICATION NUMBER: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
APPLICATION NUMBER: 08 DEC-1995
APPLICATION NUMBER: 08/566,622
APPLICATION NUMBER: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
APPLICATION NUMBER: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-708-123D-5

Query Match 11.9%; Score 79; DB 4; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62; Gaps 5;
Matches 25; Conservative 21; Nismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVWSDPTRSLTFSASLIR-ORVKVGIAELNNVSGOVSYKRPAPKEGGAD 67
Db 53 INRTASSVFTDIALNLTQTCNLTFQOLEQNYGITISG-----LPPEPKPNL-- 103

Qy 68 ACVIMPNENOSIRTIVSGAENLA---TLKAEMETHK 101
Db 104 SCIV--NEGRKMRCEWDGGRETHLETNTFLKSEWATHK 139

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/583.153A
 FILING DATE: 28-DEC-1995

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/559,485
 FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995

APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995

NAME: Meiklejohn, Anita L.
 REGISTRATION NUMBER: 35,283

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid

TOPOLOGY: unknown
 MOLECULE TYPE: protein

US-08-583-153A-5
 QUERY Match 11 9%; Score 79; DB 4; Length 488;
 Best Local Similarity 25.5%; Pred. No 0.62;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWSDPTRLSTTSASLLR-QRVKVGIAELANNSGQIVSVKRPAPKPEGC 67
 Db 53 INRTASSVFTDIALNQIITFCOLEQNYGITISG-----LPPEKPKNL-- 103

Qy 68 ACVIMPNENQSIITVVISSAENLA---TLKAEWETHK 101
 Db 104 SCIV--NEGKRNCEWDGGRETHLETNFLKSEWATHK 139

RESULT 10

US-08-525-556-4
 Sequence 4, Application US/08825558
 Patent No. 5965724

GENERAL INFORMATION:
 APPLICANT: Sharkey, Andrew A.
 INVENTION: Gp 130 Lacking the Transmembrane Domain

NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stern, Kessler, Goldstein & Fox

STREET: 110 New York Avenue
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 ADDRESSSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/638.524B
 FILING DATE: 26-APR-1996

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/599,485
 FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/018001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: unknown

MOLECULE TYPE: protein

US-08-638-524B-5
 Query Match 11.9%; Score 79; DB 4; Length 488;
 Best Local Similarity 25.5%; Pred. No 0.52;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWSDPTRLSTTSASLLR-QRVKVGIAELANNSGQIVSVKRPAPKPEGC 67
 Db 53 INRTASSVFTDIALNQIITFCOLEQNYGITISG-----LPPEKPKNL-- 103

Qy 68 ACVIMPNENQSIITVVISSAENLA---TLKAEWETHK 101
 Db 104 SCIV--NEGKRNCEWDGGRETHLETNFLKSEWATHK 139

RESULT 10

US-08-825-556-4
 Sequence 4, Application US/08825558
 Patent No. 5965724

GENERAL INFORMATION:
 APPLICANT: Sharkey, Andrew A.

INVENTION: Gp 130 Lacking the Transmembrane Domain

NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Stern, Kessler, Goldstein & Fox

STREET: 110 New York Avenue

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825,558
 FILING DATE: 19-MAR-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: EDMOND, ROBERT W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0623.05300001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 TELEX/FAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 658 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-825-558-4

Query Match 11.9%; Score 79; DB 2; Length 658;
 Best Local Similarity 25.5%; Pred. No. 0.98;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
 Qy 9 ITSTANKIIVWSDPTRLSTFSASLLR-QRVKGIAELNNVSGQYVSYKRPKPEGGAD 67
 Db 82 INRTASSVFTDIASLNQIOLTCNLTFCOLEQNYGTTISG-----LPPEPKPNL-- 132

Qy 68 ACYIMPENQNSIRTIVSQAENLA---TLKAWEETHK 101
 Db 133 SCIV--NEGKKMRCEWDGGRETHLETNFLKSEWAHK 168

RESULT 12
 US-07-797-556-2
 ; Sequence 2, Application US/07797556
 ; Patent No. 5262522
 GENERAL INFORMATION:
 APPLICANT: Gearing, David P.
 TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
 TITLE OF INVENTION: Inhibitory Factor
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/797,556
 FILING DATE: 19911122
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2607
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-587-0430
 TELEFAX: 206-587-0606
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-797-556-2

Query Match 11.9%; Score 79; DB 1; Length 708;
 Best Local Similarity 25.5%; Pred. No. 1.1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
 Qy 9 ITSTANKIIVWSDPTRLSTFSASLLR-QRVKGIAELNNVSGQYVSYKRPKPEGGAD 67
 Db 82 INRTASSVFTDIASLNQIOLTCNLTFCOLEQNYGTTISG-----LPPEPKPNL-- 132

Qy 68 ACYIMPENQNSIRTIVSQAENLA---TLKAWEETHK 101
 Db 133 SCIV--NEGKKMRCEWDGGRETHLETNFLKSEWAHK 168

RESULT 13
 US-08-308-881-2
 ; Sequence 2, Application US/08308881
 ; Patent No. 5783672
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M

Query Match 11.9%; Score 79; DB 3; Length 658;

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,881
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435.
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/249,553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-058-263-2

Query Match 11.9%; Score 79; DB 2; Length 708;
 Best Local Similarity 25.5%; Pred. No. 1.1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVWSDPTRLSITFSASLLR-ORVKVGLAEINNVSGQYVSYKRPAPKPEGCAD 67
 Db 82 INFTASSVTFDIASTNLQLTNCNLTFCQEONYVGTISG-----LPPEKPKNL-- 132

Qy 68 ACVIMPNENQSIRTVISGSAENLA---TLKAEWETIK 101
 Db 133 SCIVV-NEGKRKRCWDGREGTHELTNTFLKSEWATHK 168

RESULT 15
 US-09-059-099-2
 Sequence 2, Application US/09059099
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 CO-APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/059,099
 FILING DATE: 12-SEP-1994
 CLASIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,881
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELELEX: 756822

Query Match 11.9%; Score 79; DB 1; Length 708;
 Best Local Similarity 25.5%; Pred. No. 1.1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVWSDPTRLSITFSASLLR-ORVKVGLAEINNVSGQYVSYKRPAPKPEGCAD 67
 Db 82 INFTASSVTFDIASTNLQLTNCNLTFCQEONYVGTISG-----LPPEKPKNL-- 132

Qy 68 ACVIMPNENQSIRTVISGSAENLA---TLKAEWETIK 101
 Db 133 SCIVV-NEGKRKRCWDGREGTHELTNTFLKSEWATHK 168

RESULT 14
 US-09-058-263-2
 Sequence 2, Application US/09058263
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 CO-APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/058,263
 FILING DATE: 12-SEP-1994
 CLASIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,881
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELELEX: 756822

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OM protein - protein search, using sw model.

Run on: June 1, 2005, 09:31:22 ; search time 114 Seconds
(without alignment)

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTMQPTISTANXIVWSD.....NAGLGFGLDPTAAIVSDDTA 131

Scoring table: BL050M62

Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
Maximum Match 100\$
Listing first 45 summaries

Database : A_Geneseq_16Dec04:
1: geneseqp1980:/*
2: geneseqp1990:/*
3: geneseqp2000:/*
4: geneseqp2001:/*
5: geneseqp2002:/*
6: geneseqp2003:/*
7: geneseqp2003B:/*
8: geneseqp2004B:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	666	100.0	131	6	ABR056509	Abr056509 AP205 coa
2	666	100.0	131	6	ABU05695	Abu05695 Bacteriop
3	666	100.0	131	6	ABR44612	Abt44612 AP205 coa
4	666	100.0	131	7	ADD24203	Add24203 Bacteriop
5	666	100.0	131	7	ADJ82146	Adj82146 Protein f
6	666	100.0	131	7	ADK17202	Adk17202 AP3 prote
7	666	100.0	131	8	ADJ36392	Adj36392 Bacteriop
8	666	100.0	131	8	ADI40712	Adi40712 Bacteriop
9	666	100.0	131	8	ADJ67171	Adj67171 Bacteriop
10	666	100.0	131	8	ADR52205	Adr52205 Bacteriop
11	666	100.0	131	8	ADL98305	Adl98305 Murant Ba
12	660	99.1	131	6	ABR56508	Abt56508 AP205 coa
13	660	99.1	131	6	ABU05694	Abu05694 Bacteriop
14	660	99.1	131	6	ABR44611	Abt44611 AP205 coa
15	660	99.1	131	7	ADD24202	Add24202 Bacteriop
16	660	99.1	131	7	ADJ82145	Adj82145 Protein f
17	660	99.1	131	7	ADK17201	Adk17201 AP1 prote
18	660	99.1	131	8	ADJ36389	Adj36389 Bacteriop
19	660	99.1	131	8	ADI40710	Adi40710 Bacteriop
20	660	99.1	131	8	ADJ67170	Adj67170 Bacteriop
21	660	99.1	131	8	ADK52204	Adk52204 Bacteriop
22	660	99.1	131	8	ADL98301	Adl98301 Bacteriop
23	80	12.0	131	9	ABU05510	Abu05510 M. tuberc
24	79	11.9	329	2	AAW17859	Aaw17859 Rheumatoi
25	79	11.9	329	8	ADR14425	Adr14425 Human NP-

ALIGNMENTS

RESULT 1						
ID	ABR56509	standard; protein;	131 AA.			
XX	XX					
AC	AC					
DT	DT					
XX	28-JUL-2003	(first entry)				
DE	AP205	coat protein	SEQ ID NO:81.			
XX	XX					
KW	Antigen presenting cell; APC; immune response; virus like particle; VLP; cytostatic; virucide; antibacterial; antiparasitic; fungicide; antiallergic; immunosuppressive; antiaddictive; antiinflammatory; antithyroid; antidiabetic; neuroprotective; notropic; osteopathic; anti-rheumatic; antiarrhythmic; vaccine; immunization; infectious disease; anti-viral protection; tumour; allergy; drug addiction; Crohn's disease; graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis; Alzheimer's disease; osteoporosis; rheumatoid arthritis; inflammatory autoimmune disease.					
XX	XX					
OS	Synthetic.					
XX	XX					
PN	WO2003024480-A2.					
XX	XX					
PD	27-MAR-2003.					
XX	XX					
PF	16-SEP-2002; 2002WO-TB004232.					
XX	XX					
PR	14-SEP-2001; 2001US-0318967P.					
XX	XX					
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.					
XX	XX					
PI	Bachmann MF, Storni T, Lechner F,					
XX	XX					
WPI	2003-363095/34.					
XX	XX					
PT	A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, or immunizing or treating tumors or infectious diseases, e.g. viral infections.					
PT	PT					
PT	PT					
PS	Disclosure; Page 240-241; 243pp; English.					
XX	XX					
CC	The present invention describes a composition (C) for enhancing an immune response against an antigen or a virus-like particle in an animal. (C) comprises a virus-like particle (VLP) bound to at least one antigen, or a VLP capable of being recognised by the immune system of the animal. Also described: (1) enhancing an immune response against an antigen or a VLP					
CC	CC					
CC	CC					

PR	14-SEP-2001;	2001US-0318994P.	XX	15-JAN-2004	(first entry)
PR	22-APR-2002;	2002US-0371145P.	XX	DT	Bacteriophage AP205 coat protein #2.
XX	(CYTO-)	CYTOS BIOTECHNOLOGY AG.	XX	KW	vaccine composition; virus-like particle; core particle;
PA	(MAUR/)	MAURER P.	XX	KW	first attachment site; antigen; antigenic determinant; prion protein;
PA	(TISS/)	TISSOT A.	XX	KW	PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
PA	(SCHW/)	SCHWARZ K.	XX	KW	prion disease; Bovine Spongiform Encephalopathy; BSE;
PA	(MEIJ/)	MEIJERINK E.	XX	KW	Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
PA	(LIPO/)	LIPOWSKY G.	XX	OS	Synthetic.
PA	(PUMP/)	PUMPENS P.	XX	OS	Bacteriophage AP205.
PA	(CIEL/)	CIELENS I.	XX	PN	WO2003059386-A2.
PA	(RENH/)	RENHOF A.	XX	PD	24-JUL-2003.
PI	Maurer P.	Tissot A.	XX	XX	PT 17-JAN-2003; 2003WO-EP000460.
PI	Pumpens P.	Cielens I.	XX	PR	18-JAN-2002; 2002US-00050962.
XX	XX	XX	PR	21-JUL-2002; 2002WO-EP00166.	
PT	XX	XX	PR	08-JUL-2002; 2002US-0193728P.	
PT	XX	XX	PR	18-JUL-2002; 2002US-0196590P.	
PS	XX	XX	PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
PS	XX	XX	PA	Bachmann M., Maurer P., Pellicioli E., Renner WA;	
XX	XX	XX	PA	WPI; 2003-598483/56.	
XX	XX	XX	DR	N-PSDB; ADD42404.	
PS	XX	XX	PT	A vaccine composition for preventing or treating prion diseases (e.g. Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.	
XX	XX	XX	PT	PT Disclosure; SEQ ID NO 96; 246pp; English.	
CC	XX	XX	CC	This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigenic determinant that is a prion protein (PrP) or its dimer, or a PrP peptide, the antigenic or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or therapeutic activity. The composition is useful as a medicament or in manufacturing a medicament or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is that of a mutant RNA-phage AP205 coat protein which is related to the invention.	
CC	XX	XX	CC	Sequence 131 AA;	
CC	XX	XX	Query Match	Score 666; DB 7; Length 131;	
CC	XX	XX	Best Local Similarity	100.0%;	
CC	XX	XX	Matches 131; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MANKTMOPTISTANKIVNSDPTTRISSLTSFASLRLQRVKGIAELNNYGGQQYSVYKRPPA	Qy	1 MANKTMOPTISTANKIVNSDPTTRISSLTSFASLRLQRVKGIAELNNYGGQQYSVYKRPPA 60	
Db	1	MANKTMOPTISTANKIVNSDPTTRISSLTSFASLRLQRVKGIAELNNYGGQQYSVYKRPPA	Db	1 MANKTMOPTISTANKIVNSDPTTRISSLTSFASLRLQRVKGIAELNNYGGQQYSVYKRPPA 60	
Qy	61	KPEGCADACVIMPNENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGFLDP	Qy	61 KPEGCADACVIMENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGFLDP 120	
Db	61	KPEGCADACVIMPNENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGFLDP	Db	61 KPEGCADACVIMENOSIRTIVSGSAENLATLKAEMETHKRNVDTLFASGNAGLGFLDP 120	
Qy	121	TAATIVSSDTTA 131	Qy	121 TAATIVSSDTTA 131	
Db	121	TAATIVSSDTTA 131	Db	121 TAATIVSSDTTA 131	
RESULT 4					
ADD24203					
ID ADD24203	standard; protein; 131 AA.				
XX	ADJ82116				
ID ADJ82146	standard; protein; 131 AA.				
AC ADD24203;					

XX AC ADK17202;
 XX DT 06-MAY-2004 (first entry)
 XX DE Protein for RANKL antigen array to treat bone disease.
 XX KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 XX bone disease; encephalopathy; immune system stimulation.
 XX Unidentified.
 OS XX WO20030309225-A2.
 PN XX WO2003040164-A2.
 PD XX 15-MAY-2003.
 PF XX 07-NOV-2002; 2002WO-EPO12449.
 PR XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002US-00050902.
 PR 19-JUL-2002; 2002WO-IB000166.
 PR XX 19-JUL-2002; 2002US-0396635P.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PI XX Bachmann M, Jennings G, Sonderegger I;
 DR XX WPI; 2003-441518/41.
 PT XX Composition comprising an ordered and repetitive antigen or antigenic
 PT determinant array, useful as a medicament, or for manufacturing a
 PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 PT Hodgkin's lymphoma.
 XX Disclosure; SEQ ID NO 81; 245pp; English.
 PS XX DR; 2003-441430/41.
 XX New compositions comprising a core particle and at least one antigen or
 PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 PT of bone diseases, particularly mammalian encephalopathies.
 PS Disclosure; SEQ ID NO 113; 222pp; English.
 XX The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic
 CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, fragment or RANKL
 peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to
 CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and
 CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The
 CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.
 XX Sequence 131 AA;
 SQ Query Match 100.0%; Score 666; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTMQPTISTANKIIVNSDPTRLSTTFASLIIQRVKGIAELNNVSGQYVSYKRPAP 60
 Db 1 MANKTMQPTISTANKIIVNSDPTRLSTTFASLIIQRVKGIAELNNVSGQYVSYKRPAP 60
 QY 61 KPEGCADACVIMPNENOSIRTVISSAENLATKAEMETHKRNYDTLPSAGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPNENOSIRTVISSAENLATKAEMETHKRNYDTLPSAGNAGLGFLDP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 6
 ID ADK17202 standard; protein; 131 AA.
 XX ID ADK17202

XX ID ADK17202
 AC XX ADK17202; (first entry)
 XX DT 06-MAY-2004 (first entry)
 XX DE AP3 protein for repetitive antigen array.
 XX KW antiallergic; antiasthmatic; cytosstatic; vaccine; virus-like particle;
 KW interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
 KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
 XX Unidentified.
 OS XX WO2003040164-A2.
 PD XX 15-MAY-2003.
 PF XX .07-NOV-2002; 2002WO-EPO12455.
 PR XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR XX 19-JUL-2002; 2002US-0396635P.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PI XX Bachmann M, Jennings G, Sonderegger I;
 DR XX WPI; 2003-441518/41.
 PT XX Composition comprising an ordered and repetitive antigen or antigenic
 PT determinant array, useful as a medicament, or for manufacturing a
 PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 PT Hodgkin's lymphoma.
 XX Disclosure; SEQ ID NO 81; 245pp; English.
 PS XX The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin, and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC attachment site with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.
 XX Sequence 131 AA;
 SQ Query Match 100.0%; Score 666; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTMQPTISTANKIIVNSDPTRLSTTFASLIIQRVKGIAELNNVSGQYVSYKRPAP 60
 Db 1 MANKTMQPTISTANKIIVNSDPTRLSTTFASLIIQRVKGIAELNNVSGQYVSYKRPAP 60
 QY 61 KPEGCADACVIMPNENOSIRTVISSAENLATKAEMETHKRNYDTLPSAGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPNENOSIRTVISSAENLATKAEMETHKRNYDTLPSAGNAGLGFLDP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 7
 ID ADJ36392

ID	ADU36392	standard; protein; 131 AA.
XX	DE	Bacteriophage AP205 mutant coat protein SEQ ID NO:3.
XX	XX	virus-like particle; bacteriophage AP205; coat protein; cytostatic;
AC	XX	vaccine; gene therapy; cancer; allergy; asthma; mutant.
DT	XX	Bacteriophage AP205 coat protein virus-like particle P5T mutant.
XX	DB	antiallergic; cytostatic; virucide; immunostimulant; vaccine;
XX	XX	immune response; virus-like particle; immunostimulatory; allergy; tumour;
KW	XX	chronic disease; chronic viral disease; bacteriophage AP205;
KW	XX	coat protein; VLP; adjuvant; mutant; mitein.
KW	XX	XX
XX	OS	Bacteriophage AP205.
XX	XX	OS
XX	PN	WO200400351-A1.
PD	XX	31-DEC-2003.
XX	XX	20-JUN-2003; 2003WO-EP006541.
PP	XX	20-JUN-2002; 2002US-0389989P.
PR	XX	20-JUN-2002; 2002US-0389989P.
PA	XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA	XX	PT New virus-like particle, useful for preparing a composition for treating
PA	XX	PT or preventing a disease e.g., cancer, allergy or asthma.
PA	XX	Claim 1; SEQ ID NO 3; 170bp; English.
PS	XX	PT
PI	XX	PT
DR	XX	DR; ADI40713; ADI40834.
PS	XX	PS
PI	XX	PI; 2004-108361/11.
XX	XX	DR; 2004-108361/11.
XX	PT	New compositions comprising a virus-like particle (VLP), an
PT	PT	immunostimulatory substance bound to the VLP, and an antigen mixed with
PT	PT	the VLP, useful for enhancing immune response or for treating e.g. tumors
PT	PT	or chronic viral diseases.
XX	XX	Example 16; SEQ ID NO 93; 252pp; English.
PS	XX	The invention describes a composition for enhancing an immune response in
CC	CC	an animal comprising a virus-like particle, an immunostimulatory
CC	CC	substance bound to the virus-like particle, and an antigen mixed with the
CC	CC	virus-like particle. The composition or the vaccine is useful in the
CC	CC	manufacture of a pharmaceutical for the treatment of a disorder or
CC	CC	disease such as allergies, tumours, chronic diseases and chronic viral
CC	CC	diseases. The composition is also useful for enhancing an immune response
CC	CC	in an animal. This is the amino acid sequence of a bacteriophage AP205
CC	CC	coat protein P5T mutant, a modified virus like particle (VLP) that can be
CC	CC	used in the adjuvant of the invention.
XX	XX	Sequence 131 AA;
SQ	XX	Query Match 100.0%; Score 666; DB 8; Length 131;
Best Local Similarity	100.0%	Pred. No. 2e-72;
Matches	131;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ	XX	Sequence 131 AA;
Qy	1	MANKTMQPITSTANKIVWSDPTRLSTTSASLLRQRVKVIGIAELNNVSCQYVSYKRPAP 60
Db	1	MANKTMQPITSTANKIVWSDPTRLSTTSASLLRQRVKVIGIAELNNVSCQYVSYKRPAP 60
Qy	61	KPSEGCADVCIMPENQSRTVSGSAENLATKAIEWETHKRNDTLFASGNAGIGFLDP 120
Db	61	KPSEGCADVCIMPENQSRTVSGSAENLATKAIEWETHKRNDTLFASGNAGIGFLDP 120
Qy	121	TAATVSSDPTA 131
Db	121	TAATVSSDPTA 131
RESULT 8		
ADU36392	ADU36392	standard; protein; 131 AA.
XX	XX	XX
AC	AC	AC
DT	DT	DT
XX	XX	XX
RESULT 9		
ADI40712	ADI40712	standard; protein; 131 AA.
ID	ID	ID
XX	XX	XX
AC	AC	AC
DT	DT	DT
XX	XX	XX
RESULT 10		
ADI40712	ADI40712	standard; protein; 131 AA.
ID	ID	ID
XX	XX	XX
AC	AC	AC
DT	DT	DT
XX	XX	XX

RESULT 11		61 KPEGGADACVIMPENNQSIRTVISSENAENLATLAKAWEWTHKRNDTFLASGNAGLGFLDP 120
ID ADL98305	XX	ADL98305 standard; protein; 131 AA.
AC	XX	
DT	18-NOV-2004	(first entry)
DB	Mutant Bacteriophage AP205 coat protein.	
XX	XX	
XX	KW	hapt-en-carrier conjugate; recombinant virus protein; attachment site;
XX	KW	drug addiction; fentanyl; heroin; morphine; amphetamine; cocaine;
XX	KW	methyleneidoxymethylamphetamine; methamphetamine; methylphenidate;
XX	KW	nicotine; cocaine; noracetone; PCP; LSD; mescaline; psilocybin;
XX	KW	tetrahydrocannabinol; diazepam; desipramine; imipramine; nortriptyline;
XX	KW	amitriptyline; coat protein; mutant; mutant protein.
OS	OS	Bacteriophage AP205.
OS	Synthetic.	
XX	Key	Location/Qualifiers
EH	FH	Misc-difference 5
FT	FT	/note= "Wild type Pro replaced by Thr"
FT	FT	
XX	W02004009116-A2.	
PN	XX	
PD	XX	
PD	PP	29-JAN-2004.
XX	XX	18-JUL-2003; 2003WO-EP007850.
PR	XX	18-JUL-2002; 2002US-0396575P.
PA	PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA	PA	
XX	XX	Bachmann MF, Maurer P,
PI	PI	XX
XX	DR	WPI; 2004-132865/13.
XX	DR	N-PSDB; ADL98306.
XX	XX	The invention comprises a hapt-en-carrier conjugate for treating or preventing addiction to drug, comprises core particle having first attachment site and hapt-en with second attachment site linked to form ordered and repetitive conjugate.
PT	PT	Example 9; SEQ ID NO 18; 144p; English.
PT	PT	The invention comprises a hapt-en-carrier conjugate consisting of a carrier (e.g. a recombinant virus protein) that has at least one attachment site, and at least one second attachment site. The method of the invention is useful for treating or preventing addiction to a drug, such as: codeine, fentanyl, heroin, morphine, amphetamine, cocaine, methylenedioxymethamphetamine, methamphetamine, methylphenidate, nicotine, cocaine, normocaine, PCP, LSD, mescaline, psilocybin, tetrahydrocannabinol, diazepam, desipramine, imipramine, nortriptyline and the amitriptyline class of drugs. The method of the invention is also useful for preventing and treating diseases associated with addiction. The present amino acid sequence was used in an example of the invention.
PS	XX	Sequence 131 AA;
SQ	XX	Query Match 100.0%; Score 666; DB 8; Length 131; Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 131; Conservative 0;		
Qy	1	MANKTMDPITSTANKIVWSDPTRLSTTSFASLLQRVKGIAELNNVSGQYTVSKRDP 60
Db	1	MANKTMDPITSTANKIVWSDPTRLSTTSFASLLQRVKGIAELNNVSGQYTVSKRDP 60
Qy	2	KPGCDAACVIMPENOSRTVIGSAAENLATLAKAWEWTHKRNDTFLASGNAGLGFLDP 120

CC represent sequences used in the exemplification of the present invention
 XX Sequence 131 AA;

Sequence Match 99.1%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1..le-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MANKMQPTISTANKIIVNSDPPTRLSTTFASASLIRQRVKVIAELNNVSGOYVSVYKRPA 60
 Db 1 MANKMQPTISTANKIIVNSDPPTRLSTTFASASLIRQRVKVIAELNNVSGOYVSVYKRPA 60
 Qy 61 KPEGCADAVCYMPHENOSIRTIVIGSAENLATKAEMETHKRNDTTLFASGNAGLGFDP 120
 Db 61 KPEGCADAVCYMPHENOSIRTIVIGSAENLATKAEMETHKRNDTTLFASGNAGLGFDP 120
 Qy 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 Qy 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 13

ID ABU09694 standard: protein; 131 AA.
 XX ABU09694;

XX DT 03-JUL-2003 (first entry)
 XX DE Bacteriophage AP205 coat protein.
 XX KW Bacteriophage AP205; coat protein; hypotensive; cerebroprotective;
 cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; interarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage.
 XX OS Bacteriophage AP205.
 XX PN WO2003031466-A2.
 XX PD 17-APR-2003.
 XX PF 07-OCT-2002; 2002WO-EP011219.

XX PR 05-OCT-2001; 2001US-031699BP.
 PR 07-NOV-2001; 2001US-0311045P.
 PR 18-JAN-2002; 2002US-03050902.
 PR 21-JAN-2002; 2002WO-1B000165.
 PR 19-JUL-2002; 2002US-0396637P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PI Bachmann M;
 XX WPI; 2003-430264/40.
 DR N-PDB; ABX95223.

XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 or infarction.
 XX Disclosure: Page 96; 97pp; English.
 PS The invention describes an angiotensin peptide moiety carrier conjugate
 CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal

CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC for producing antibodies. This is the amino acid sequence of a
 CC bacteriophage AP205 coat protein used in the preparation of the vaccine
 CC conjugates of the invention
 XX SQ Sequence 131 AA;

Query Match 99.1%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1..le-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MANKMQPTISTANKIIVNSDPPTRLSTTFASASLIRQRVKVIAELNNVSGOYVSVYKRPA 60
 Db 1 MANKMQPTISTANKIIVNSDPPTRLSTTFASASLIRQRVKVIAELNNVSGOYVSVYKRPA 60
 Qy 61 KPEGCADAVCYMPHENOSIRTIVIGSAENLATKAEMETHKRNDTTLFASGNAGLGFDP 120
 Db 61 KPEGCADAVCYMPHENOSIRTIVIGSAENLATKAEMETHKRNDTTLFASGNAGLGFDP 120
 Qy 61 KPEGCADAVCYMPHENOSIRTIVIGSAENLATKAEMETHKRNDTTLFASGNAGLGFDP 120
 Db 61 KPEGCADAVCYMPHENOSIRTIVIGSAENLATKAEMETHKRNDTTLFASGNAGLGFDP 120
 Qy 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 Qy 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 14

ID ABR44611 standard: protein; 131 AA.
 XX AC ABR44611;

XX AC ABR44611;
 XX DT 25-JUL-2003 (first entry)
 XX DE AP205 coat protein SEQ ID NO:80.
 XX KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
 XX OS Synthetic.
 XX PN WO2003024481-A2.
 XX PD 27-MAR-2003.
 XX PF 16-SEP-2002; 2002WO-1B004132.
 XX PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR-) MAURER P.
 PA (TISS-) TISSOT A.
 PA (SCHW-) SCHWARZ K.
 PA (MEIJ-) MEIJERINK E.
 PA (LIPO-) LIPOWSKY G.
 PA (POMP-) POMPENS P.
 PA (CIEL-) CIELENS I.
 PA (RENH-) RENHOFA R.

XX PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhoffa R, Bachmann MF, Storni T;
 XX DR WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT - viral infections.
 XX Disclosure; Page 319; 322pp; English.
 PS

XX The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance. The immunostimulatory substance is bound to the VLP. Also described: (1) enhancing an immune response in an animal by introducing (C) into the animal; (2) Producing (C) for enhancing an immune response in an animal; (3) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; and (4) immunising or treating an animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (c) boosting a T cell response in the animal by administering the vaccine. (C) has immunostimulant, cytostatic, anticancer, antiallergic, varicide and antibacterial activities. (1) can be used in vaccines for enhancing an immune response in an animal, particularly a mammal or human. Specifically, (C) is useful for enhancing a B cell response, a T cell response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine comprising (C) can also be used for immunising or treating an animal, e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, reptiles or fish. (C) is particularly useful in prophylactic or therapeutic vaccines against allergies, tumours (e.g. breast cancers, neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis, measles or chicken pox), or bacterial infections (e.g. tuberculosis, pneumonia or syphilis). ACC69790 to AC69815 and ABR44502 to ABR44612 represent sequences used in the exemplification of the present invention

XX Sequence 131 AA;

Score 660; DB 6; Length 131;

Best Local Similarity 99.1%; Pred. No. 1.1e-71; Mismatches 0; Indels 1; Gaps 0;

Matches 130; Conservative 0; MisMatches 1; Delins 0; Gaps 0;

Qy 1 MANKTMDPITSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP 60.

Db 1 MANKPMQPITSSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP 60

Qy 61 KPGCGADAVIMPNENOSIRTIVSGSAENLATKAENWETHKRNDTLFASGNAGLGFLDP 120

Db 61 KPGCGADAVIMPNENOSIRTIVSGSAENLATKAENWETHKRNDTLFASGNAGLGFLDP 120

Qy 121 TAIIVSSDTTA 131

Db 121 TAIIVSSDTTA 131

RESULT 15
ADD24202 ID ADD24202 standard; protein; 131 AA.
XX AC ADD24202;
XX DT 15-JAN-2004 (first entry)

DE DE Bacteriophage AP205 coat protein #1.
XX KW vaccine composition; virus-like particle; core particle;
KW first attachment site; antigen; antigenic determinant; prion protein;
KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
KW prion disease; Bovine Spongiform Encephalopathy; BSE;
KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.

XX OS Bacteriophage AP205.

XX PN WO2003059386-A2.

XX PD 24-JUL-2003.

XX PF 17-JAN-2003; 2003WO-BP000460.

XX PR 18-JAN-2002; 2002US-00050902.

PR 08-JUL-2002; 2002WO-1000166.

PR 18-JUL-2002; 2002US-0193725P.

XX PR 18-JUL-2002; 2002US-0396590P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Pellicoli E, Renner WA;

PI DR WPI; 2003-598483/56.
XX N-PSDB; ADD24201.

XX PT A vaccine composition for preventing or treating prion diseases (e.g. Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

XX PS Disclosure; SEQ ID NO 95; 246pp; English.

XX CC This invention relates to a novel vaccine comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (PrP) or its dimer, or a PrP peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is that of a RNA-phage AP205 coat protein which is related to the invention.

SQ Sequence 131 AA;

	Query Match	Score	DB	Length
Qy	1 MANKTMDPITSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP	99.1*	660	131;
Db	1 MANKPMQPITSSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP	99.2*	60	130;
Qy	1 MANKPMQPITSSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP	99.2*	60	130;
Db	1 MANKPMQPITSSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP	99.2*	60	130;
Qy	1 KPGCGADAVIMPNENOSIRTIVSGSAENLATKAENWETHKRNDTLFASGNAGLGFLDP	61	120	
Db	1 KPGCGADAVIMPNENOSIRTIVSGSAENLATKAENWETHKRNDTLFASGNAGLGFLDP	61	120	
Qy	121 TAIIVSSDTTA 131	121	131	
Db	121 TAIIVSSDTTA 131	121	131	

Best Local Similarity 99.1%; Pred. No. 1.1e-71; Mismatches 0; Indels 1; Gaps 0;

Best Local Similarity 99.2%; Pred. No. 1.1e-71; Mismatches 0; Indels 0; Gaps 0;

Conservative 0; MisMatches 1; Delins 0; Gaps 0;

Qy 1 MANKTMDPITSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP 60

Db 1 MANKPMQPITSSTANKIIVNSDPTRLSTTFSASLILQRVRKGIAEINNNYSGQQYVSVYKRPAP 60

Qy 61 KPGCGADAVIMPNENOSIRTIVSGSAENLATKAENWETHKRNDTLFASGNAGLGFLDP 120

Db 61 KPGCGADAVIMPNENOSIRTIVSGSAENLATKAENWETHKRNDTLFASGNAGLGFLDP 120

Qy 121 TAIIVSSDTTA 131

Db 121 TAIIVSSDTTA 131

Search completed: June 1, 2005, 09:41:59
Job time : 114 secs

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ATTACHMENT C

RESULTS
NUMBER OF HITS SATISFYING CHOSEN PARAMETERS: 283416
SEARCHED: 2010-09-22 10:00:00
SEARCHER: MIGRANTO

post-processing: Minimum Match 0% Maximum Match 100%
-
hypothetical protein b24850 - mycobacterium replicans
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72877

Listing first 45 summaries

Database : PIR_79.*

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B112: 3: Dir3: *

P113: D114:*

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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	80	12.0	194	hypothetical protein -
2	79	11.8	918	pitstatin IVWS-DPTRLSTTSASLARQRVRYGIAELANNVSSQQYVSYK- - -RPAF 60 membrane glycoprotein -
3	78	11.7	305	pitstatin IVWS-DPTRLSTTSASLARQRVRYGIAELANNVSSQQYVSYK- - -RPAF 60 membrane glycoprotein -
4	76.5	11.5	546	KEPGCADAVIMENQNSIRTIVSGSAENLATIKAWEWETHKRANDTLFASAGNIGFLDP 120 membrane glycoprotein -
5	75.5	11.3	519	KEPGCADAVIMENQNSIRTIVSGSAENLATIKAWEWETHKRANDTLFASAGNIGFLDP 120 membrane glycoprotein -
6	73.5	11.0	213	acetylcholine receptor -
7	73.5	11.0	291	probable enoyl-coa acyltransferase -
8	73.5	11.0	831	ORFA of Listeria ssp. maloactic enzyme -
9	73	10.9	547	A36337 membrane glycoprotein gp130 precursor - human
10	72	10.8	273	membrane glycoprotein gp130 precursor - human
11	70.5	10.6	414	C;Species: Homo sapiens (man) C;Accession: A36337
12	70.5	10.6	646	C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
13	70.5	10.6	217631	C;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
14	70	10.5	26926	A;Reference number: A36337; MUID:91084844; PMID:2261637
15	70	10.5	519	A;Accession: A36337
16	69.5	10.4	519	A;Status: Preliminary
17	69.5	10.4	319	A;Molecule type: mRNA
18	69.5	10.4	358	A;Residues: 1-918 <H1B>
19	69.5	10.4	643	A;Cross-references: UNIPROT:P40189; GB:M57230; NID:9186353; PMID:AA59155_1; P
20	69.5	10.4	942	A;Gene: IL6ST; GP130
21	69	10.4	1078	A;Map position: 5q11-q11
22	69	10.3	270415	A;Genetics:
23	69	10.3	562	A;Protein name: glycoprotein membrane protein
24	69	10.3	666	A;Cross-references: 5q11-q11
25	68	10.2	252	A;Map position: 5q11-q11
26	68	10.2	297762	A;Protein name: membrane protein
27	68	10.2	350	A;Cross-references: 5q11-q11
28	67.5	10.1	551494	A;Protein name: membrane protein
29	67.5	10.1	330	A;Cross-references: 5q11-q11
30	67.5	10.1	577	A;Protein name: membrane protein

A;Note: sequence extracted from NCBI backbone (NCBIN:126968, NCBIP:126970)
C;Superfamily: chaperonin groEL
C;Keywords: molecular chaperone

Query Match 11.8%; Score 79; DB 2; Length 918;
Best Local Similarity 25.5%; Pred. No. 9.3; Gaps 5;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIYWSDPTRLSTFSASLIR-ORVKVKGIAELNNVSGOVSYKRPAPKPEGCCAD 67
Db 82 INRTASSVTFDTIASLNQLTCNLTFGGLEQVNQYGITISG-----LPPEKPKNL-- 132

Qy 68 ACVIMPNNENOSIRTIVSGAENLA----TILKAEMETHK 101
Db 133 SCIV--NEGRKMRCEWDGGRETHLETFNLKSEWATHK 168

RESULT 3
A75334 [acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75334
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; PMID:10567266; PIDN:AAA6896; PIDN:AAA30351.1; PID:9162601; PIDN:AAA30351.1; PID:9162602
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <WHI>
A;Cross-references: UNIPROT:Q9RT24; GB:AE002033; GB:AE000513; NID:96459726; PMID:6517904
A;Experimental source: strain R1
C;Genetics:

A;Gene: DR1945
A;Maf position: 1
C;SuperFamily: [acyl-carrier-protein] S-malonyltransferase; [acyl-carrier-protein] S-malonyltransferase; coenzyme A
C;Keywords: acyltransferase; coenzyme A
F;7267/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;93/Active site: Ser (covalent substrate-binding) #status predicted
F;198/Active site: His #status predicted

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 3.1; Gaps 4;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

Qy 13 ANKTIYWSDPTRLSTFSASLIR-ORVKVKGIAELNNVSGOVSYKRPAPKPEGCCADACYI 71
Db 103 AGVITFLDRLR-TRKRGEMMQAVPEGTAMSAMGD-----PAVAEVRAQAQGV 154

Qy 72 MP-NENQSIIRTVISSAENLATLKAEWEIHKRNVTDLFFASGNAGLGFDPAAIVSSDT 130
Db 155 QPANENAPQTQVISSEKAADAASELKTRGLKAIPLKYSAPFHICALMRPAAGLSAIIH 214

Qy 131 A 131
Db 215 A 215

RESULT 4
B47073 chaperonin GroEL - Chromatium vinosum
C;Species: Chromatium vinosum
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B47073
R;Perreyra, R.G.; Soncini, F.C.; Viale, A.M.
J.; Bacteriol. 175, 1514-1523, 1993
A;Title: Cloning, characterization, and functional expression in Escherichia coli of cha
A;Reference number: A47073; PMID:8444812
A;Accession: B47073
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-546 <FER>
A;Cross-references: UNIPROT:P31293; GB:M99443; NID:9145007; PIDN:AAA23319.1; PID:9145009

Qy 3 NKPMQPTSTANKI-YWSDPTRLSTFSASLIR-ORVKVKGIAELN-----NVS 48
Db 68 NMGAQMVKEVAKSTSDIAGDGTATVLAQAMVREGIKAVAGMNPMDLRKGMDKAVEAA 127

Qy 49 GQYVSYKRPAPKPEGCCADACYIIMPENOSIRTIVSGAENL--ATLKAEMETHKRNVD 105
Db 128 TBLKDKSKPCKPAPMAQVGTTISANSDDSIGTIAZAMEKYGKEGVITVEDGTSNL 187

Qy 106 TLPGNGNAGLGFDP 120
Db 188 DVVEGMQFDRGVILSP 202

RESULT 5
A75334 [acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - bovine acetylcholine receptor - bovine
C;Species: Bos primigenius taurinus (cattle)
C;Accession: I45847
R;Takai, T.; Noda, M.; Furutani, Y.; Takahashi, H.; Notake, M.; Shimizu, S.; Kayano, T.;
Eur. J. Biochem. 143, 109-115, 1984
A;Title: Primary structure of gamma subunit precursor of calf-muscle acetylcholine receptor
A;Reference number: I45847; MUID:84285374; PMID:6517904
A;Accession: I45847
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-519 <TAK>
A;Cross-references: UNIPROT:P13536; GB: M28307; PID:9162601; PIDN:AAA30351.1; PID:9162602
C;Genetics:
C;Gene: AChR
C;Keywords: acetylcholine receptor

Query Match 11.3%; Score 75.5; DB 2; Length 519;
Best Local Similarity 22.0%; Pred. No. 11; Gaps 6;
Matches 37; Conservative 21; Mismatches 59; Indels 51; Gaps 6;

Qy 4 KPKPI-----TSTANKIVWSDPTRLSTFSASLIR-ORVKVIA-----EL 44
Db 360 RPLAPAVQDAHPRLQNSSSGPITAGEEVAVLCLPSSELLPRQRQNGLYRAALEKLEK 419

Qy 45 NNTSGQ--YVSVTKRPAPKPEGCCADACVIMPNENQSIRTIVSGAENLATLKAEWEIHK 101
Db 420 GPESGQSPEWCGSLKQAPAIQAVCAECLNLIARHOOHTFDISGN-----DPTAIVSSD 471

Qy 102 RNVD-----TLPASNAIGLFL-----DPTAIVSSD 128
Db 472 RVLDRCFLAMLSLFVGCTAGIFIMAHYNRVPALPFPDRSYLIPSSD 519

RESULT 6
D70972 probable enoyl-coA hydratase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Accession: D70972
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Ratnandimla, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome of the bacterium
A;Reference number: A70500; MUID:9829587; PMID:9634230
A;Accession: D70972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA	A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Residues: 1-213 <COL>	A; Accession: AC1515
A; Cross-references: UNIPROT:O50402; GB:AL000198; PIDN:g3242262; NID:93242262; PIDN:CAA1575	A; Status: preliminary
A; Experimental source: Strain H37RV	A; Molecule type: DNA
A; Gene: echa18	A; Cross-references: UNIPROT:Q92DZ6; GB:AL592022; PIDN:GAC95897_1; PIDN:GAC95897_1; PID:916413105; GSPDB:G
C; Superfamily: Naphthoate synthase	C; Experimental source: strain Clip11262
Query Match 11.0%; Score 73.5; DB 2; Length 213;	C; Genetics:
Best Local Similarity 27.6%; Pred. No. 5.8;	A; Gene: lin0665
Matches 24; Conservative 14; Mismatches 42; Indels 7; Gaps 3;	
Qy 33 LRQRVKVGAELNNVSGQYSV---YKRPAKPEGGCADAVIMPENQSIRTIVSGSAE 88	Query Match 11.0%; Score 73.5; DB 2; Length 831;
Db 1 MRREAMTKNDDEASNPCCGGDIEAEMCQLMREQQPAEGVDRVALQRHRNVALITLUSHPOAQ 60	Best Local Similarity 25.8%; Pred. No. 30;
Qy 89 NLATLKAEEWTHKRNVTIIFASGNAGL 115	Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;
Db 61 NALNL-ASWRRLRKLDDLI--AGESGL 84	Qy 8 PITSTAN-KIVTWSDPTRLSTTSFASSLRQRVKVGAELNNVSGQ---YVSVYKRAP--- 60
RESULT 7	Db 646 PLVSDNDKVRKGVPEDSYETLNA-----YNEDGVRAEAKTFIVRLKSPAPII 694
T51668 myb-related transcription factor MYB61 [imported] - Arabidopsis thaliana (fragment)	Qy 61 -KPGEGCADAVIMPENQSIRTIVSGSAENLATL---KREWETHKRNVTIIFASGNAGL 113
C; Species: Arabidopsis thaliana (mouse-ear cress)	Db 695 TVDPEVSYDSAAI-KNETELLEKVRAKTNDSAITSADPKYKWTFCGSYTVTLNAVNE 753
C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004	Qy 114 GLGFIDPPTAAIV 125
C; Accession: T51668	Db 754 GIP-ABEVTFIV 764
R; Krantz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J. Paz-Ares, J.; Weissenbar, B.	RESULT 9
Plant J. 16, 263-276, 1998	AC1314
A; Title: Towards functional characterisation of the members of the R2R3-MYB gene from Arabidopsis thaliana (mouse-ear cress)	malolactic enzyme (malate dehydrogenase)
A; Reference number: 214349; MUID:9839469	C; Species: Listeria monocytogenes
A; Accession: T51668	C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
A; Status: preliminary; translated from GB/EMBL/DBJ	C; Accession: AC1314
A; Cross-references: UNIPROT:Q9SB99; EMBL:AF062896; PIDN: AAC83618.1	R; Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A; Experimental source: cultivar Columbia	A; Reference number: AB1077; MUID:21537279; PMID:11679669
C; Genetics:	A; Accession: AC1314
A; Gene: MYB61	A; Status: preliminary
A; Map position: I	A; Molecule type: DNA
C; Key words: transcription factor	A; Cross-references: 1-547 <GLA>
Query Match 11.0%; Score 73.5; DB 2; Length 291;	A; Experimental source: strain EGDe
Best Local Similarity 23.0%; Pred. No. 8.4;	C; Genetics:
Matches 32; Conservative 19; Mismatches 67; Indels 21; Gaps 5;	C; Gene: lin01915
Qy 3 NKPQMPITSTANK--IVNSDPTRLSTTSFASSLRQRVKVGAELNNV-----G 49	C; Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)
Db 76 NDHKSPSSATNQDFELPSPSISDYFQKLNFSNLGILSVTTDSLCSMIPQFQSG 135	Query Match 10.0%; Score 73; DB 2; Length 547;
Qy 50 QTV-SVYKRPAKPEGGCADAVIMPENQSIRTIVSGSAENLATLKAEEWTHKRNVTIIF 108	Best Local Similarity 25.0%; Pred. No. 20;
Db 136 NMVQSVLQTPV---CYKPSVAPHDNSSSPRTSGGDHVKLAPRNWFQTNNNNNTSNFP 190	Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;
Qy 109 ASGENAGLGFIDPPTAAIVSS 127	Qy 12 TANKTWSDPTRLSTTSFASSLRQRVKVGAELNNVSGQYVSVYKRAP----PEGC 65
Db 191 -DNGGFSWSPNSSTS 207	Db 191 TNNETLNDPLYG-----NRPRRLSESBYDATASFVNKEVEPKTLHWDGGR 242
RESULT 8	Qy 66 ADACTIMPENQSIRTV---ISGS----ASNLATKAEEWTHKRNVTIIFASGNAGLGP 117
A11515 ORFA of Listeria seeligeri, (LPXTG motif) homolog lin0665 [imported] - Listeria innocua	Db 243 ANASRLHNRYDKICFTNDDIQGTGMMVVAATLQVSRIPLSEQKIIIFAGTAGTGI 302
C; Species: Listeria innocua	Qy 118 LDPTTAIVSSDT 129
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	Db 303 ADQLSSQLMRET 314
R; Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.	RESULT 10
Science 294, 849-852, 2001	B6446
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.	formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - Methanococcus jannaschii
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996	Species: Methanococcus jannaschii
C; Accession: A11515	C; Date: 13-Sep-1996 #text_change 16-Aug-2004

C;Accession: B64446
 R;Built; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J; Beich, C.I.; Overbeek, R.; Kirnness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Larson, J.D.; Sedow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 C;Species: Chlorella virus PBCV-1
 C;Accession: T17631
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T17631
 C;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:868807
 A;Accession: B64446
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Residues: 1-273 <BUL>
 A;Cross-references: UNIPROT:Q58571; GB:U67558; GB:L77117; NID:91591786; PIDN:AAB99173.1;
 C;Superfamily: Formylmethanofuran dehydrogenase, subunit C
 C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten
 A;Map position: FOR110572-1111393
 A;Genetics:
 C;Genetics:
 A;Map position: FOR110572-1111393
 C;Superfamily: Formylmethanofuran dehydrogenase, subunit C
 C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten

Query Match 10.8%; Score 72; DB 2; Length 273;
 Best Local Similarity 27.6%; Pred. No. 11;
 Matches 27; Conservative 14; Mismatches 31; Indels 26; Gaps 4;

Qy 34 RQRVKGV---IAEINNVSGGVSVYKRPK-----PEGGADACVIMPNEN 76
 Db 43 RKRIVADDFDVELNDIEGSEPRIVKNSPKLXIGSKMTKGIVVEG-DAGMYVGAEW 100

Qy 77 QSTRUVISSAENLATLKAEWETHKRNVTOLFEASGNAG 114
 Db 101 KGGKLVVNGNAES-----WAGONMKGGEBLLIKGNAG 131

RESULT 11

A86229
 hypothetical protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A86229
 R;Theoretical
 R;Ecker, J.J.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, R.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Salzberg, S.L.; Schwartz, J.R.; Shiota, P.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:11130712
 A;Accession: A86229
 A;Residues: 1-414 <STO>
 A;Cross-references: UNIPROT:Q9SAV9; GB:AE005172; NID:93482929; PIDN: AAC33214.1; GSPDB:GN
 C;Genetics:
 A;Map position: 1
 C;Superfamily: petunia myb-related protein 1; myb DNA-binding repeat homology

Query Match 10.6%; Score 70.5; DB 2; Length 414;
 Best Local Similarity 23.0%; Pred. No. 26;
 Matches 32; Conservative 18; Mismatches 68; Indels 21; Gaps 5;

Qy 3 NKPMDPITANK--IVWSDPTRLSTTFASLIRQRVKYGIAEINNS-----G 49
 Db 151 NDHKSPSSSATNQDFELLRPSDLSDYFGQKLNFNSNLGLSVDSSCSMPPQQFSPG 210

Qy 50 QRY-SVYKRPAKPGEGCADACVIMENENQSRTVYGSAAENLATLKAEMTHERGRNVTDF 108
 Db 211 NMVGSVLQTPV----CVERPSISLPPDNNSSSPISGGDEVLRAPNTEQTNNNNTSNFF 265

RESULT 12

T17631
 hypothetical protein A140R - Chlorella virus PBCV-1
 C;Species: Chlorella virus PBCV-1
 C;Accession: T17631
 C;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:868807
 A;Accession: T17631
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Cross-references: UNIPROT:Q84460; EMBL:U42580; NID:94028896; PIDN: AAC96508.1
 A;Experimental source: specific host Chlorella strain NC64A
 A;Genetics:
 A;Note: A140R

Query Match 10.6%; Score 70.5; DB 2; Length 646;
 Best Local Similarity 24.8%; Pred. No. 45;
 Matches 26; Conservative 15; Mismatches 33; Indels 31; Gaps 5;

Qy 4 KPMQPPI-----TSTANCI-LRQRYKVG---IAETANN 46
 Db 500 KPTAPVGIIIAAKVTAVPNANKVSLQYTKPKNKLTKVTVKTHGMKVGEAVDVVVRNK 559

Qy 47 VSGOYVSYK---RPARPKPEG-----CADAIVIMPNNQ 77
 Db 560 DPYAFAVYKKGA1KPAKPGKPTAPAGTIVIAAKYTAVPNTNK 604

RESULT 13

I38344
 titin, cardiac muscle [validated] - human
 N;Alternate names: connectin
 N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)

C;Species: Homo sapiens (man)
 C;Accession: I38344; T138345; S20898; S20897; S20899; S63565; S37393
 R;Labelit, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A;Reference number: A57430; MUID:96026330; PMID:7569978
 A;Accession: I38344
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A;Molecule type: mRNA
 A;Residues: 1-26926 <LAB1>
 A;Cross-references: UNIPROT:Q10466; EMBL:X90568; NID:91017424; PMID:91017425
 A;Accession: I38345
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1977-2014 <MUS>
 A;Cross-references: EMBL:X63270; NID:9602579; PIDN:CAA58243.1; PID:9602580
 R;Labelit, S.; Gauteil, M.; Keyey, A.; Trinick, J.
 EMBO J. 11, 1711-1716, 1992
 A;Title: Towards a molecular understanding of titin.
 A;Reference number: S20897; MUID:92258380; PMID:1582406
 A;Accession: S20898
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 13597-14200; 'I' 14202-14696 <LAB2>
 A;Cross-references: EMBL:X64698; NID:937192; PIDN:CAA45939.1; PID:937193
 A;Accession: S20897
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 16330-16382; 'S' 16384-16756; 'F' 16758-16860 <LAB3>
 A;Cross-references: EMBL:X64699; NID:937190; PIDN:CAA45940.1; PID:937191

A;Accession: S20899

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 'P,'22278-'22431,'R,'22433-'22448,'G,'22450-'22453,'Q,'22455-'22480,'TR,'22483-'2

A;Cross-references: EMBL:X64697; NID:937190; PID:CAA45988.1;

R;Kohlmeier, B.; Olivieri, N.; Witt, C.C.; Hermann, B.G.; Labey, S.

J. Mol. Biol. 256, 556-563, 1996

A;Title: Genomic organization of M line titin and its tissue-specific expression in two

A;Reference number: S66665; MUID:9617761; PMID:8604138

A;Accession: S63665

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 26729-26825 <COL>

A;Cross-references: EMBL:X92412; NID:91236761

R;Gautel, M.; Leonard, K.; Labelle, S.

EMBO J. 12, 3827-3834, 1993

A;Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentiat

A;Reference number: S37393; MUID:94008990; PMID:8404852

A;Accession: S37393

A;Molecule type: mRNA

A;Residues: 26831-26926 <GAU>

R;Impronta, S.; Pastore, A.S.; Pastore, A.

Submitted to the Brookhaven Protein Data Bank, February 1996

A;Reference number: A67376; PDB:1JIT

A;Contents: annotation; conformation by (1)H-NMR, residues 5253-5341

R;Pfuhl, M.; Pastore, A.

Submitted to the Brookhaven Protein Data Bank, August 1996

A;Reference number: A67201; PDB:1NCT

A;Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155

C;Keywords:

A;Gene: GDB:TTN

A;Cross-references: GDB:127867; OMIM:188840

A;Map position: 2q31-2q32

A;Function:

A;Description: structural protein forming filaments in striated muscle

C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pro

C;Keywords: alternative splicing; cofilin binding; cardiac muscle; duplication; glyco

structural protein

R;24752-2500/Domain: protein kinase homology <KIN>

F;8-84, 177, 905, 2276, 2378, 2459, 2481, 2563, 2669, 2895, 3088, 3179, 3384, 3432, 3628, 3772, 4058,

98, 11066, 11486, 11515, 11635, 11949, 12170, 12478, 12875, 13001, 13036, 132940, 1

status predicted

F;16780, 16972, 17057, 17602, 17667, 17681, 18120, 18188, 18209, 18336, 18670, 18680, 18

21900, 21935, 22295, 22455, 22627, 22897, 23024, 23318, 23983, 24012, 24177, 24290, 24447, 24642, 248

F;26170, 26170, 26184, 26190/Binding site: phosphate (Ser) (covalent) #status experimental

Qy 4 KPMOPITSANKIWYSDPPRL---STTFPASL-LRQRVKG---IAEINNNVSGQ----50

Db 16073 KPIIPIQWIKGDQBLNTARLEIKSTDFTSLSVQDAVFDGNYLTKAKNNGERSVTY 16132

RESULT 14

S13874

nicotinic acetylcholine receptor gamma chain precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: S13874; S03082

R;Witzemann, V.; Barg, B.; Konno, T.; Koenen, M.; Kues, W.; Criado, M.; Hofmar

Bur. J. Biochem. 194, 437-441, 1990

A;Title: Primary structure and functional expression of the alpha-, beta-, gamma-, delta

A;Reference number: S13872; MUID:9109317; PMID:1702709

A;Accession: S13874

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-519 <WIT>

A;Cross-references: UNIPROT:P18916; EMBL:X74834;

R;Witzemann, V.; Barg, B.; Nishikawa, Y.; Sakmann, B.; Numa, S.

FEBS Lett. 223, 104-112, 1987

A;Title: Differential regulation of muscle acetylcholine receptor gamma- and epsilon-sub

A;Reference number: S03081; MUID:8803021; PMID:3666131

A;Accession: S03082

A;Molecule type: DNA

A;Reference number: I5566; MUID:86308110; PMID:3755765

A;Accession: S20899

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-519 <RES>

A;Cross-references: UNIPROT:M00012; PID:92000012

R;Yu, L.; Lapolla, R. J.; Davidson, N.

Nucleic Acids Res. 14, 3525-3552, 1986

A;Title: Mouse muscle nicotinic acetylcholine receptor gamma-subunit: cDNA sequence and

A;Reference number: A24919; MUID:86205253; PMID:310242

A;Accession: A24919

A;Molecule type: mRNA

A;Residues: 1-230, 'V, 232-345, 'L, 347-519, 'X, <YUL>

A;Note: the authors translated the codon ARG for residue 116 as His

R;Gardner, P.D.; Heinemann, S.; Patrick, J.

Brain Res. 3, 69-76, 1987

A;Title: Transcriptional regulation of nicotinic acetylcholine receptor genes: identification

A;Reference number: A43774

A;Accession: A43774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-57 <GAR>

A;Cross-references: GB: M27455; PID:9191613

R;Crowder, C.M.; Merlie, J.P.

Mol. Cell. Biol. 8, 5257-5267, 1988

A;Title: Stepwise activation of the mouse acetylcholine receptor delta- and gamma-subunit

A;Reference number: I49457; MUID:89218986; PMID:3243354

A;Accession: I49457

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: GB: M27455; PID:9191613

R;Crowder, C.M.; Merlie, J.P.

Mol. Cell. Biol. 8, 5257-5267, 1988

A;Title: Stepwise activation of the mouse acetylcholine receptor gamma chain #status predicted <MAT>

A;Reference number: I49457

A;Accession: I49457

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-18 <RE2>

A;Cross-references: GB: M22381; PID:9191597; PMID:9553854

C;Genetics:

A;Introns: 19/1

A;Note: 1 list of introns may be incomplete

C;Superfamily: acetylcholine receptor

C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

C;Domain: signal sequence #status predicted <SG>

F;23-519/Product: nicotinic acetylcholine receptor gamma chain #status predicted

Query Match 10.5%; Score 70; DB 2; Length 519;

Best Local Similarity 25.7%; Pred. No. 38; Mismatches 38; Indels 26; Gaps 4;

Matches 27; Conservative 14; MisMatches 14; GapPos 38; Indels 26; Gaps 4;

Qy 29 SASIURQVKVGTAE----IANN----LNN----VSGQVSVTKRPAPKPEGCADACVIMPNENQS 78

Db 397 SELFRQNGIVQAVIBKLENGPEVRQSFBGSLRQASPAIQACVDACNLMARARQ 456

Qy 79 IRTVISSAENLATLKAEMETHKRNDV-----TLPASGNGL 115

Db 457 QSHFDSGN-----EEWLLVGRVLLDRVCFLAMSLSPICGPAGI 493

RESULT 15

S13874

nicotinic acetylcholine receptor gamma chain precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: S13874; S03082

R;Witzemann, V.; Barg, B.; Konno, T.; Koenen, M.; Kues, W.; Criado, M.; Hofmar

Bur. J. Biochem. 194, 437-441, 1990

A;Title: Primary structure and functional expression of the alpha-, beta-, gamma-, delta

A;Reference number: S13872; MUID:9109317; PMID:1702709

A;Accession: S13874

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-519 <WIT>

A;Cross-references: UNIPROT:P18916; EMBL:X74834;

R;Witzemann, V.; Barg, B.; Nishikawa, Y.; Sakmann, B.; Numa, S.

FEBS Lett. 223, 104-112, 1987

A;Title: Differential regulation of muscle acetylcholine receptor gamma- and epsilon-sub

A;Reference number: S03081; MUID:8803021; PMID:3666131

A;Accession: S03082

A;Molecule type: DNA

page 6

A;Residues:	203-306	<W12>
A;Cross-references:	EMBL:X06364; NID:955588; PID:CAA29662-1; PID:955589	
C;Superfamily:	acetylcholine receptor	
C;Keywords:	glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane	
F;39-65.Domain:	transmembrane #status predicted <TM1> F;72-90.Domain:	transmembrane #status predicted <TM2>
Query Match	10.5%	Score: 70; DB: 2; Length: 519;
Best Local Similarity	25.8%	Pred. No: 389
Matches	31	Conservative 13; Mismatches 46; Indels 30; Gaps 5;
Qy	18	WSDPTP R --LSTTPESASLIRQPKVGF E --IIN N --VSGQYVSVKRPKPE 63
Db	382	WPNTTRECGDLCLRSELLFRQRGNGVQAVL K LEKLGPMRQSDFCGSLKQASPAIQ 441
Qy	64	GCA D ACVIMPNENGSIRIVTGSMENIATLKA W ETHRANVD D --TUFASGNAGL 115
Db	442	ACUDACNIMARAHHQSHFD S GN D --ETWLLVGRVLDPRVCFLAMLSIFCIGTAGI 493

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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:38:08 ; Search time 91 Seconds

(without alignments)
497.627 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKMQPTSTANKIVSWS.....NAGLGFELDPTAAIVSSTDVTA 131

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters:

1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications At:*

1: /cgn2_6/ptodata/1/pubpaa/us070 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/pctaa/us070 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/us070 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/us060 PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/pctaa/us070 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/pctaa/us070 NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/us080 NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/us090 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/us090A PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/us090B PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/us090C PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/us090 NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/us10A PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/us10B PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/us10C PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/us10D PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/us11A NEW PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/us11A NEW PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/us60 NEW PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/us60A PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	14 US-10-243-739-80	Sequence 80, Appl
2	668	100.0	131	14 US-10-244-065-80	Sequence 80, Appl
3	668	100.0	131	14 US-10-289-454-80	Sequence 80, Appl
4	668	100.0	131	15 US-10-346-190-95	Sequence 95, Appl
5	668	100.0	131	15 US-10-465-811-90	Sequence 90, Appl
6	668	100.0	131	15 US-10-289-456-112	Sequence 112, Appl
7	668	100.0	131	15 US-10-617-064-14	Sequence 14, Appl
8	668	100.0	131	15 US-10-622-124-28	Sequence 1, Appl
9	668	100.0	131	15 US-10-617-876-1	Sequence 28, Appl
10	668	100.0	131	16 US-10-622-087-28	Sequence 28, Appl
11	660	98.8	131	14 US-10-243-739-81	Sequence 81, Appl
12	660	98.8	131	14 US-10-244-065-81	Sequence 81, Appl
13	660	98.8	131	14 US-10-289-454-81	Sequence 81, Appl

\$ Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	US-10-243-739-80	Sequence 80, Application US/10243739
		; Publication No. US20030091593A1
		; GENERAL INFORMATION:
		; APPLICANT: Bachmann, Martin F.
		; APPLICANT: Scorni, Tazio
		; APPLICANT: Lechner, Franziska
		; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of Immune Responses Induced by Virus Like Particles
		; FILE REFERENCE: 1700.021001
		; CURRENT APPLICATION NUMBER: US/10/243,739
		; PRIORITY FILING DATE: 2002-09-16
		; NUMBER OF SEQ ID NOS: 73
		; SOFTWARE: PatentIn version 3.1
		; SEQ ID NO 80
		; LENGTH: 131
		; TYPE: PRT
		; ORGANISM: Artificial Sequence
		; FEATURE:
		; OTHER INFORMATION: AP205 coat protein

Query Match Best Local Similarity 100.0%; Pred. No. 7.9e-71; Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPITSTANKIVSWS.....NAGLGFELDPTAAIVSSTDVTA 60

Db 1 MANKPMQPITSTANKIVSWS.....NAGLGFELDPTAAIVSSTDVTA 60

QY 61 KPEGCADACIMPNENQSRITYISGSAENLATKAWEWTHKRNYDTLPGASGNAGLFDP 120

Db 61 KPEGCADACIMPNENQSRITYISGSAENLATKAWEWTHKRNYDTLPGASGNAGLFDP 120

RESULT 2

Qy 121 TAAIVSSDTA 131
; Sequence 80, Application US/102444065
; Publication No. US20030093668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tisbot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerad
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhoffa, Regina

; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles

; FILE REFERENCE: 1700_0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,945
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein

US-10-244-065-80

Query Match 100.0%; Score 668; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPTSTANKIVNSDPTRLSTTFASLIRQRVKVIAELNNYSGQQYVSYKRPA 60
Db 1 MANKPMQPTSTANKIVNSDPTRLSTTFASLIRQRVKVIAELNNYSGQQYVSYKRPA 60

Qy 61 KPEGCADACVIMPNENQSRTVISGSAENLATIKAEWETHKRNDTLFASGNAGLFDP 120
Db 61 KPEGCADACVIMPNENQSRTVISGSAENLATIKAEWETHKRNDTLFASGNAGLFDP 120

Qy 121 TAAIVSSDTA 131
Db 121 TAAIVSSDTA 131

RESULT 3

Qy 121 TAAIVSSDTA 131
; Sequence 80, Application US/10289454
; Publication No. US2003015479A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Gary
; APPLICANT: Sondergaard, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases

; FILE REFERENCE: 1700_0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-01-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21

US-10-289-454-80

Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPTSTANKIVNSDPTRLSTTFASLIRQRVKVIAELNNYSGQQYVSYKRPA 60
Db 1 MANKPMQPTSTANKIVNSDPTRLSTTFASLIRQRVKVIAELNNYSGQQYVSYKRPA 60

Qy 61 KPEGCADACVIMPNENQSRTVISGSAENLATIKAEWETHKRNDTLFASGNAGLFDP 120
Db 61 KPEGCADACVIMPNENQSRTVISGSAENLATIKAEWETHKRNDTLFASGNAGLFDP 120

Qy 121 TAAIVSSDTA 131
Db 121 TAAIVSSDTA 131

US-10-289-456-112

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Query Match          100.0%;  Score 668;  DB 15;  Length 131;
Best Local Similarity 100.0%;  Pred. No. 7.9e-71;
Matches 131;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60
Db      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60

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RESULT 5

US-10-465-811-90

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; Sequence 90, Application US/10465811
; Publication No. US2014000533BA1
; GENERAL INFORMATION:
;   APPLICANT: BACHMANN, MARTIN F
;   APPLICANT: RENNER, WOLFGANG A
;   TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS
;   TITLE OF INVENTION: METHOD OF PREPARATION AND USE THEREOF
;   FILE REFERENCE: 1700-029004
;   CURRENT APPLICATION NUMBER: US/10/465, 811
;   CURRENT FILING DATE: 2003-06-20
;   PRIOR APPLICATION NUMBER: US 60/389, 898
;   PRIOR FILING DATE: 2002-06-20
;   NUMBER OF SEQ ID NOS: 131
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO: 90
;   LENGTH: 131
;   TYPE: PCT
;   ORGANISM: Bacteriophage AP205
;   US-10-465-811-90

Query Match          100.0%;  Score 668;  DB 15;  Length 131;
Best Local Similarity 100.0%;  Pred. No. 7.9e-71;
Matches 131;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60
Db      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60

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US-10-465-811-90

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; Sequence 90, Application US/10465811
; Publication No. US2014000533BA1
; GENERAL INFORMATION:
;   APPLICANT: BACHMANN, MARTIN F
;   APPLICANT: RENNER, WOLFGANG A
;   TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS
;   TITLE OF INVENTION: METHOD OF PREPARATION AND USE THEREOF
;   FILE REFERENCE: 1700-029004
;   CURRENT APPLICATION NUMBER: US/10/465, 811
;   CURRENT FILING DATE: 2003-06-20
;   PRIOR APPLICATION NUMBER: US 60/389, 898
;   PRIOR FILING DATE: 2002-06-20
;   NUMBER OF SEQ ID NOS: 131
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO: 90
;   LENGTH: 131
;   TYPE: PCT
;   ORGANISM: Bacteriophage AP205
;   US-10-465-811-90

Query Match          100.0%;  Score 668;  DB 15;  Length 131;
Best Local Similarity 100.0%;  Pred. No. 7.9e-71;
Matches 131;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60
Db      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60

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RESULT 6

US-10-289-456-112

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; Sequence 112, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
;   APPLICANT: BACHMANN, MARTIN
;   APPLICANT: Soohn, Gunther
;   TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
;   FILE REFERENCE: 1700-0330001
;   CURRENT APPLICATION NUMBER: US/10/289, 456
;   CURRENT FILING DATE: 2002-11-07
;   PRIOR APPLICATION NUMBER: PCT/IB02/00166
;   PRIOR FILING DATE: 2002-01-21
;   PRIOR APPLICATION NUMBER: US 10/050, 902
;   PRIOR FILING DATE: 2002-01-18
;   PRIOR APPLICATION NUMBER: US 60/396, 635
;   PRIOR FILING DATE: 2002-07-19
;   PRIOR FILING DATE: 2001-11-07
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO: 112
;   LENGTH: 131
;   TYPE: PCT
;   ORGANISM: Artificial Sequence
;   FEATURE: OTHER INFORMATION: AP205 coat protein
;   OTHER INFORMATION: AP205 coat protein

Query Match          100.0%;  Score 668;  DB 15;  Length 131;
Best Local Similarity 100.0%;  Pred. No. 7.9e-71;
Matches 131;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60
Db      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60

```

RESULT 7

US-10-622-064-14

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; Sequence 14, Application US/10622064
; Publication No. US2004005909A1
; GENERAL INFORMATION:
;   APPLICANT: Bachmann, Martin F
;   APPLICANT: Maurer, Patrick F
;   TITLE OF INVENTION: Haptens-Carrier Conjugates and Uses Thereof
;   FILE REFERENCE: 1700-0300001
;   CURRENT APPLICATION NUMBER: US/10/622, 064
;   CURRENT FILING DATE: 2003-07-18
;   PRIOR APPLICATION NUMBER: US 60/396, 575
;   PRIOR FILING DATE: 2002-07-18
;   NUMBER OF SEQ ID NOS: 33
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO: 14
;   LENGTH: 131
;   TYPE: PCT
;   ORGANISM: Bacteriophage AP205
;   US-10-622-064-14

Query Match          100.0%;  Score 668;  DB 15;  Length 131;
Best Local Similarity 100.0%;  Pred. No. 7.9e-71;
Matches 131;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60
Db      1 MANKPMQPTSTANKIIVWSDPTRLSTTSASLRLQRVKVGLAELNNVSGQYVSYKRPAP 60

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RESULT 8

US-10-617-876-1

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; Sequence 1, Application US/10617876
; Publication No. US2004007661A1
; GENERAL INFORMATION:
;   APPLICANT: Bachmann, Martin F
;   APPLICANT: Tisot, Alain
;   APPLICANT: Pumpens, Paul
;   APPLICANT: Cielens, Indulis
;   APPLICANT: Renhofa, Regina
;   TITLE OF INVENTION: Molecular Antigen Arrays
;   FILE REFERENCE: 1700-031001
;   CURRENT APPLICATION NUMBER: US/10/617, 876
;   CURRENT FILING DATE: 2003-07-14
;   PRIOR APPLICATION NUMBER: US 60/396, 126
;   PRIOR FILING DATE: 2002-07-17

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NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-617-876-1

Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; SEQ ID NO 28
; Software: PatentIn version 3.2

Qy 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
Db 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-087-28

Query Match 100.0%; Score 668; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; SEQ ID NO 28
; Software: PatentIn version 3.2

Qy 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
Db 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-087-28

Query Match 100.0%; Score 668; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; SEQ ID NO 28
; Software: PatentIn version 3.2

Qy 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
Db 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-087-28

Query Match 100.0%; Score 668; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; SEQ ID NO 28
; Software: PatentIn version 3.2

Qy 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
Db 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-087-28

RESULT 9
US-10-622-124-28
; Sequence 28, Application US/10222124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Fuluri, Alina
; TITLE OF INVENTION: Għrel-in-Carrier Conjugates
; FILE REFERENCE: 1700_0340001
; CURRENT APPLICATION NUMBER: US/10-622-124
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,638
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-124-28

Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; SEQ ID NO 28
; Software: PatentIn version 3.2

Qy 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
Db 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-81

Query Match 98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70; Indels 0; Gaps 0;
Matches 130; Conservative 1; Mismatches 0; SEQ ID NO 28
; Software: PatentIn version 3.1

Qy 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
Db 1 MANKPMQPITSTANKIVWDSDPTRLSTTFASLIRQVKVIAELANNVSGQQYVSVYKRPA 60
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-81

RESULT 10
US-10-622-087-28
; Sequence 28, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Tissot, Alain
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias

Db 121 TAAIVSSDDTA 131
 RESULT 12
 US-10-244-065-81
 ; Sequence 81, Application US/10244065
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin P.
 ; APPLICANT: Storni, Tazio
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Tisbet, Alain
 ; APPLICANT: Schwarz, Katrin
 ; APPLICANT: Meijerink, Edwin
 ; APPLICANT: Lipowsky, Gerad
 ; APPLICANT: Pumpens, Paul
 ; APPLICANT: Cielens, Indulis
 ; APPLICANT: Renhoffa, Regina
 ; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
 ; FILE REFERENCE: 1700_0220001
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 60/374,145
 ; PRIOR FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: 60/318,994
 ; PRIOR FILING DATE: 2001-09-14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 91
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: AP205 coat protein
 ; US-10-244-065-81

Query Match 98.8%; Score 660; DB 14; Length 131;
 Best Local Similarity 99.2%; Pred. No. 7e-70; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKPMOPTSTANKIVSWSDPTRSLSTSASLLRQRVKGIAELNNYSGQYVSYKRPA 60
 Db 1 MANKTMOPITSTANKIVSWSDPTRSLSTSASLLRQRVKGIAELNNYSGQYVSYKRPA 60
 Qy 61 KPEGCADACVIMENQNSRTVSGSAENLATIKAEMETHKRNVDTLFPASGNAGLGFDP 120
 Db 61 KPEGCADACVIMENQNSRTVSGSAENLATIKAEMETHKRNVDTLFPASGNAGLGFDP 120
 Qy 121 TAAIVSSDDTA 131
 Db 121 TAAIVSSDDTA 131

RESULT 14
 US-10-346-190-96
 ; Sequence 96, Application US/10346190
 ; Publication No. US20030219459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Pelliccioli, Erica
 ; APPLICANT: Renner, Wolfgang A.
 ; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
 ; FILE REFERENCE: 1700_0290003
 ; CURRENT FILING DATE: 2003-01-17
 ; PRIOR APPLICATION NUMBER: 60/396,590
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/393,725
 ; PRIOR FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: 60/3050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; NUMBER OF SEQ ID: NOS: 164
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 96
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: RNA-phage AP205
 ; US-10-346-190-96

Query Match 98.8%; Score 660; DB 15; Length 131;
 Best Local Similarity 99.2%; Pred. No. 7e-70; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKPMOPTSTANKIVSWSDPTRSLSTSASLLRQRVKGIAELNNYSGQYVSYKRPA 60
 Db 1 MANKTMOPITSTANKIVSWSDPTRSLSTSASLLRQRVKGIAELNNYSGQYVSYKRPA 60
 Qy 61 KPEGCADACVIMENQNSRTVSGSAENLATIKAEMETHKRNVDTLFPASGNAGLGFDP 120
 Db 61 KPEGCADACVIMENQNSRTVSGSAENLATIKAEMETHKRNVDTLFPASGNAGLGFDP 120
 Qy 121 TAAIVSSDDTA 131

RESULT 13
 US-10-289-454-81
 ; Sequence 81, Application US/10289454
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Jennings, Gary
 ; APPLICANT: Sonderseger, Ivo
 ; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
 ; FILE REFERENCE: 1700_0360001
 ; CURRENT APPLICATION NUMBER: US/10/289,454
 ; CURRENT FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: US 60/3396,636
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 10/050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/331,045

Db 121 TAAIVSSDDTA 131

RESULT 15
 US-10-465-811-93
 ; Sequence 93, Application US/10465811
 ; Publication No. US20040005338A1.
 ; GENERAL INFORMATION:
 ; APPLICANT: BACHMANN, MARTIN F
 ; APPLICANT: RENNER, WOLFGANG A
 ; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
 ; TITLE OF INVENTION: METHOD OF PREPARATION AND USE
 ; FILE REFERENCE: 1700_0290004
 ; CURRENT APPLICATION NUMBER: US/10/465,811
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 93
 ; LENGTH: 131
 ; TYPE: PR
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Bacteriophage AP205 mutant
 US-10-465-811-93

Query Match 98.8%; Score 660; DB 15; Length 131;
 Best Local Similarity 99.2%; Pred. No. 7e-70; 0;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MANKPMQPTSTANKIVWDPTRLSTTFSASLLRQVKGIAELNNSGQYNSVYKRPA P 60
 Db 1 MANKTMQPTSTANKIVWDPTRLSTTFSASLLRQVKGIAELNNSGQYNSVYKRPA P 60
 Qy 61 KPEGCADACVIMPNENOSIRTVISGSAENLATIKAEWETHKRNDTLPASGNAGLGFIDP 120
 Db 61 KPEGCADACVIMPNENOSIRTVISGSAENLATIKAEWETHKRNDTLPASGNAGLGFIDP 120
 Qy 121 TAAIVSSDDTA 131
 Db 121 TAAIVSSDDTA 131

Search completed: June 1, 2005, 09:50:59
 Job time : 92 secs

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Gencore version 5.1.6

OM protein - protein search, using sw mode1.

Run on: June 1, 2005, 09:35:42 ; Search time 30 Seconds (without alignment)

Scoring table: BLOSUM62 Gapext 0.5

Searched: 513545 seqs, 74619064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgnd2_6_ptodata/1/iaa/5A_COMBO.pep:
 2: /cgnd2_6_ptodata/1/iaa/5B_COMBO.pep:
 3: /cgnd2_6_ptodata/1/iaa/6A_COMBO.pep:
 4: /cgnd2_6_ptodata/1/iaa/6B_COMBO.pep:
 5: /cgnd2_6_ptodata/1/iaa/PCUTS_COMBO.pep:
 6: /cgnd2_6_ptodata/1/iaa/backfiles1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	11.8	332	4 US-09-313-942-10	Sequence 10, Appli
2	79	11.8	488	2 US-08-599-455B-5	Sequence 5, Appli
3	79	11.8	488	3 US-09-069-781B-5	Sequence 5, Appli
4	79	11.8	488	3 US-09-137-132-5	Sequence 5, Appli
5	79	11.8	488	3 US-08-864-564A-5	Sequence 5, Appli
6	79	11.8	488	4 US-09-094-410-5	Sequence 5, Appli
7	79	11.8	488	4 US-08-708-123D-5	Sequence 5, Appli
8	79	11.8	488	4 US-08-583-153A-5	Sequence 5, Appli
9	79	11.8	488	4 US-08-638-524B-5	Sequence 4, Appli
10	79	11.8	658	2 US-08-825-558-5	Sequence 4, Appli
11	79	11.8	658	3 US-09-312-611-4	Sequence 4, Appli
12	79	11.8	708	1 US-07-797-556-2	Sequence 2, Appli
13	79	11.8	708	2 US-08-308-881-2	Sequence 2, Appli
14	79	11.8	708	2 US-09-058-263-2	Sequence 2, Appli
15	79	11.8	708	3 US-09-058-264-2	Sequence 2, Appli
17	79	11.8	708	4 US-09-455-962-2	Sequence 2, Appli
18	79	11.8	709	5 PCT-IS95-16530-2	Sequence 7, Appli
19	79	11.8	859	4 US-09-313-942-7	Sequence 6, Appli
20	79	11.8	918	2 US-08-925-558-6	Sequence 6, Appli
21	79	11.8	918	3 US-09-312-611-6	Sequence 3, Appli
22	79	11.8	918	4 US-09-853-180B-3	Sequence 9, Appli
23	79	11.8	951	4 US-09-313-942-9	Sequence 2, Appli
24	79	11.8	1158	4 US-09-313-942-26	Sequence 26, Appli
25	79	11.8	1168	4 US-09-313-942-24	Sequence 24, Appli
26	79	10.9	488	4 US-09-252-991A-28535	Sequence 28535, Appli
27	72	10.8	185	4 US-09-252-991A-31599	Sequence 31599, Appli

ALIGNMENTS

RESULT 1
US-09-313-942-10
; Sequence 10, Application US/09313942
; Patent No. 647179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313, 942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313, 942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101, 858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-10

Query Match 11.8% ; Score 79; DB 4; Length 332;
Best Local Similarity 25.5%; Prod. No. 0.36; Indels 36; Gaps 5;
Matches 25; Conservative 21; Mismatches 36;

Qy 9 INSTANKIWSPTTRISTPSASLRL-QRVKVKGIAELNNVSQYVSYKRPAPKGEGAD 67
Db 82 INRTASSVFTDIASTNLQTCNLTFCOLEQNYGTTISG----LPPSKPKNLU-- 132

Qy 68 ACVIMPNNQNSRTVTISSAENA---TLKABWEATHK 101
Db 133 SCIV--NEGKKRNCEWDGGRETHLETNLKSEWATHK 168

RESULT 2
US-08-559-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 597621
; GENERAL INFORMATION:
; APPLICANT: Tariaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culipper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE BODY WEIGHT USING THE OB RECEPTOR
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street

CITY: Boston
 STATE: MA
 COUNTY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/599,455B
 FILING DATE: 22-JAN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/503,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph. D., Anita L.
 REGISTRATION NUMBER: 35,383
 REFERENCE/DOCKET NUMBER: 07334/017001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-599-455B-5

Query Match 11.8%; Score 79; DB 2; Length 488;
 Best Local Similarity 25.5%; Pred. No 0.64;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWSDPTRLSTPSASLLR-QPVKGIAELNNVGQVSVYKRPAPKEGGAD 67
 Db 53 INRTASSVFTDIASLNQITCNLTFCOLEQNYGTTISG-----LPPEKPKNL-- 103

Qy 68 ACVIMPNNENOSIRTVSGSAENLA---TLKAEWETHK 101
 Db 104 SCIV--NEGKMRCEWDGGRETHLETNFLKSEWATHK 139

RESULT 3
 US-09-069-781B-5
 Sequence 5, Application US/09069781B
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE DIAGNOSTICS AND TREATMENT OF BODY WEIGHT DISORDERS,
 TITLE OF INVENTION: THE DIAGNOSTS AND TREATMENT OF BODY WEIGHT DISORDERS,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/069,781B
 FILING DATE: 29-APRIL-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/864,564
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: US 08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: US 08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: US 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: US 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: US 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: US 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: US 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: US 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/082001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-069-781B-5

Query Match 11.8%; Score 79; DB 3; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0.64;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWSDPTRLSTPSASLLR-QPVKGIAELNNVGQVSVYKRPAPKEGGAD 67
 Db 53 INRTASSVFTDIASLNQITCNLTFCOLEQNYGTTISG-----LPPEKPKNL-- 103

Qy 68 ACVIMPNNENOSIRTVSGSAENLA---TLKAEWETHK 101
 Db 104 SCIV--NEGKMRCEWDGGRETHLETNFLKSEWATHK 139

RESULT 4
 US-09-137-132-5
 Sequence 5, Application US/09137132
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.
 APPLICANT: White, David W.
 APPLICANT: Tartaglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE DIAGNOSTS AND TREATMENT OF BODY WEIGHT DISORDERS,
 TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:

COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/137,132
 FILING DATE: 18-AUG-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/864,564
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: 08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: 08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/510,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Melklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/019004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-137-132-5

Query Match 11.8%; Score 79; DB 3; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0.64;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
 GENERAL INFORMATION:
 9 ITSTANKIVWSDPTRLSTFSASLLR-ORVKVGTAEILNNVSGQYVSVYKRPAPKPEGGAD 67
 Db 53 INRTASSVFTDIAASLNQLTNCNLTFCQLEQVYGTISG-----LPPERKPNL-- 103

Qy 68 ACVIMPNENOSIRTIVSGAENLA---TLKAEMETHK 101
 Db 104 SCIV-NECKKORCEWDGGRETHLETNTLKSEWATHK 139

RESULT 5
 US-08-864-564A-5
 ; Sequence 5, Application US/08864564A
 ; Patent No. 6395498
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; APPLICANT: Tepper, Robert I.
 ; APPLICANT: Culpepper, Janice A.
 ; APPLICANT: White, David W.
 ; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 ; THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 ; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,564A
 FILING DATE: 28-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: 08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Melklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/019004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-864-564A-5

Query Match 11.8%; Score 79; DB 3; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0.64;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
 GENERAL INFORMATION:
 Qy 9 ITSTANKIVWSDPTRLSTFSASLLR-ORVKVGTAEILNNVSGQYVSVYKRPAPKPEGGAD 67
 Db 53 INRTASSVFTDIAASLNQLTNCNLTFCQLEQVYGTISG-----LPPERKPNL-- 103

Qy 68 ACVIMPNENOSIRTIVSGAENLA---TLKAEMETHK 101
 Db 104 SCIV-NECKKORCEWDGGRETHLETNTLKSEWATHK 139

RESULT 6
 US-09-094-410-5
 ; Sequence 5, Application US/09094410
 ; Patent No. 640552
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; APPLICANT: Tepper, Robert I.
 ; APPLICANT: Culpepper, Janice A.
 ; APPLICANT: White, David W.
 ; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 ; THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 ; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.

ADDRESSSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/094,410
 FILING DATE: 09-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/864,564
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: 08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: 08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: 08/559,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/559,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/019003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-094-410-5

Query Match 11.8%; Score 79; DB 4; Length 488;
 Best Local Similarity 25.5%; Pred. No. 0.64; Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVWSDPTRLSTRFSASLLR-ORVKVGIAELNNVSGQVSVYKRPAPKPEGAD 67
 Db 53 INRTASSVTFDIASLNITQTCNLITFCQLEQNVTGTTISG-----LPPEKPKNL-- 103

Qy 68 ACVIMPNENQSIRTIVSGAENLA---TIIKAEMETHK 101
 Db 104 SCTV--NECKKMRCEWDGGRETHLETNFTLKSEWATHK 139

RESULT 8
 US-08-583-153A-5
 Sequence 5, Application US/08583153A
 Patent No. 6506877
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 ATTORNEY: Tapper, Robert I.
 APPLICANT: Culpepper, Janice A.
 ATTORNEY: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING TITLE OF INVENTION: OBESITY AND CACHEXIA
 NUMBER OF SEQUENCES: 41

RESULT 7
 US-08-708-123D-5
 Sequence 5, Application US/08708123D
 Patent No. 6482327
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 ATTORNEY: Tapper, Robert I.
 APPLICANT: Culpepper, Janice A.
 ATTORNEY: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING TITLE OF INVENTION: OBESITY AND CACHEXIA
 NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/638,524B
 FILING DATE: 26-APR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Melklejohn, Anita L.
 REGISTRATION NUMBER: 35,283
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 07334/018001
 TELEPHONE: 617-542-5070
 TELEX: 200154
 TELEFAX: 617-542-8906

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

US-08-583-153A-5

Query Match 9 ITSTANKIWSDPTRLSTSFSASLIR-
 Best Local Similarity 11.8%; Score 79; DB 4; Length 488;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Db 53 INRTASSVFTDIALNLQTCNLITFGCQLEQNYGTTISG-----LPPSKPKNL-- 103

Query 68 ACVIMPNENQSIIRTVISSAENA---TLKAEWETHK 101

Db 104 SCIV--NEGKKNRCEWDGGRETHILETNFLKSEWATHK 139

RESULT 10 US-08-524B-5

RESULT 9 US-08-638,524B-5

Sequence 5, Application US/08618524B
 ; Patent No. 6548669

GENERAL INFORMATION
 APPLICANT: Tartaglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
 DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB

TITLE OF INVENTION: CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825,558
 FILING DATE: 19-MAR-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: ESMOND, ROBERT W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0623.05300001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 658 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-825-558-4

Query Match 11.8%; Score 79; DB 2; Length 658;
 Best Local Similarity 25.5%; Pred. No. 1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIIVSDPPISTFSASLIR-ORVKVGAELNNVSGOYVSVKRPARKPEGGAD 67
 Db 82 INRTASSVTFDIASLNQLTCNLTFGQLEQNYGTTISG-----LPPEPKRNLL-- 132

Qy 68 ACVIMPENQSIIRTIVSSAENLA---TLKAEMETHK 101
 Db 133 SCIV--NEGKORCEWDGGRETHLETNFTLKSEWATHK 168

RESULT 11
 US-09-312-611-4
 Sequence 4, Application US/09312611
 PATENT NO. 6380160
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/312,611
 FILING DATE: 17-MAY-1999
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: ESMOND, ROBERT W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0623.05300002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 658 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-312-611-4

Query Match 11.8%; Score 79; DB 3; Length 658;

Best Local Similarity 25.5%; Pred. No. 1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIIVSDPPISTFSASLIR-ORVKVGAELNNVSGOYVSVKRPARKPEGGAD 67
 Db 82 INRTASSVTFDIASLNQLTCNLTFGQLEQNYGTTISG-----LPPEPKRNLL-- 132

Qy 68 ACVIMPENQSIIRTIVSSAENLA---TLKAEMETHK 101
 Db 133 SCIV--NEGKORCEWDGGRETHLETNFTLKSEWATHK 168

RESULT 12
 US-07-797-556-2
 Sequence 2, Application US/07797556
 PATENT NO. 526232
 GENERAL INFORMATION:
 APPLICANT: Gearing, David P.
 TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
 NUMBER OF INVENTION: Inhibitory Factor
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/797,556
 FILING DATE: 19911122
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2607
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-587-0430
 TELEFAX: 206-587-0506
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-07-797-556-2

Query Match 11.8%; Score 79; DB 1; Length 708;
 Best Local Similarity 25.5%; Pred. No. 1.1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIIVSDPPISTFSASLIR-ORVKVGAELNNVSGOYVSVKRPARKPEGGAD 67
 Db 82 INRTASSVTFDIASLNQLTCNLTFGQLEQNYGTTISG-----LPPEPKRNLL-- 132

Qy 68 ACVIMPENQSIIRTIVSSAENLA---TLKAEMETHK 101
 Db 133 SCIV--NEGKORCEWDGGRETHLETNFTLKSEWATHK 168

RESULT 13
 US-08-308-881-2
 Sequence 2, Application US/08308881
 PATENT NO. 5783672
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,881
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/249,553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-308-881-2

Query Match 11.8%; Score 79; DB 1; Length 708;
 Best Local Similarity 25.5%; Pred. No. 1.1;
 Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVWSDPTRLSTFSASLLR-QRVKVIAELNNVSGOVSYKRPAPKPEGCAD 67
 Db 82 INRTASSVTFDTIASLNLQTCNLTGQLEQNYVGTISG-----LPPEPKRNLL- 132
 Qy 68 ACVIMPNENQSIRTVISSAENIA---TILKAEWETHK 101
 Db 133 SCIVV--NEGKRNRCEWDGGRETHLETNLKSEWATHK 168

RESULT 14
 US-09-058-263-2
 Sequence 2, Application US/09058263
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 ATTORNEY: Cozman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/059,099
 FILING DATE: 12-SEP-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,881
 FILING DATE: 12-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,171
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-059-099-2

Query Match 11.8%; Score 79; DB 2; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSPANKTWSDPPLSTFSASLIR-ORVKVIAELANNVSGOYVSYKRPARKPEGCAD 67
Db 82 INRPAASSVFTEDIASLNICQLTCNULFEGLEQNYGTTISG-----LPPEPKPNL-- 132

Qy 68 ACVIMPNEAQOSIRATVSGAENIA---TLKAEWETHK 101
Db 133 SCIV--NEGKMRCEWDGGRETHILETNFTLKSSEATHK 168

Search completed: June 1, 2005, 09:47:52
Job time : 32 secs

Copyright (C) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model.
Run on: June 1, 2005, 09:31:22 : Search time 114 Seconds
(without alignment)
444 .435 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668 Sequence: 1 MANKMQPITSTANCKVWSD.....NAGLGFLLDPTAATIVSDDTA 131

Scoring table: BLOSUM62

Gapext 0.5

Searched:

2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:
1: geneseqp1980*: *
2: geneseqp1990*: *
3: geneseqp2000*: *
4: geneseqp2001*: *
5: geneseqp2002*: *
6: geneseqp2003*: *
7: geneseqp20039*: *
8: geneseqp2004*: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	6 ABR56508	ABR56508 AP205 coa
2	668	100.0	131	6 ABU09694	Abu09694 Bacteriop
3	668	100.0	131	6 ABR44611	ABR44611 AP205 coa
4	668	100.0	131	7 ADD24202	ADD24202 Bacteriop
5	668	100.0	131	7 ADJ82145	ADJ82145 Protein f
6	668	100.0	131	7 ADK17201	ADK17201 API prote
7	668	100.0	131	8 ADJ36389	ADJ36389 Bacteriop
8	668	100.0	131	8 ADI40710	ADI40710 Bacteriop
9	668	100.0	131	8 ADJ67170	ADJ67170 Bacteriop
10	668	100.0	131	8 ADK52204	ADK52204 Bacteriop
11	668	100.0	131	8 ADL98301	ADL98301 Bacteriop
12	660	98.8	131	6 ABR56509	ABR56509 AP205 coa
13	660	98.8	131	6 Abu09695	Abu09695 Bacteriop
14	660	98.8	131	6 ABR44612	ABR44612 AP205 coa
15	660	98.8	131	7 ADD24203	ADD24203 Bacteriop
16	660	98.8	131	8 ADJ82146	ADJ82146 Protein f
17	660	98.8	131	7 ADK17202	ADK17202 AP3 prote
18	660	98.8	131	8 ADJ36392	ADJ36392 Bacteriop
19	660	98.8	131	8 ADJ40712	ADI40712 Bacteriop
20	660	98.8	131	8 ADJ67171	ADI67171 Bacteriop
21	660	98.8	131	8 ADK52205	ADK52205 Bacteriop
22	660	98.8	131	8 ADL98305	ADL98305 Mutant Ba
23	80	12.0	194	5 ABU05510	Abu05510 M. tuberc
24	79	11.8	329	2 AAU17859	Aau17859 Rheumatol
25	79	11.8	329	8 ADJ14425	ADJ14425 Human NF-

RESULT 1
ID ABR56508 standard; protein; 131 AA.
XX ABR56508;
AC XX DT 28-JUL-2003 (first entry)
XX DE AP205 coat protein SEQ ID NO:80.
XX KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
cyostatic; virucide; antibacterial; anti-parasitic; fungicide;
KW immunosuppressive; anti-addictive; antilipidemic;
antihypertensive; antidiabetic; neuroprotective; nocropic; osteopathic;
KW anti-allergic; antiarthritic; vaccine; immunisation; infectious disease;
anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
graft-versus-host disease; Grave's disease; diabetes; rheumatoid arthritis;
KW Alzheimer's disease; osteoporosis; inflammatory autoimmune disease;
KW XX OS Synthetic.

RESULT 1
ID ABR56508 standard; protein; 131 AA.
XX WO2003024480-A2.
XX PN WO2003024480-A2.
PD 27-MAR-2003.
XX 16-SEP-2002; 2002WO-1B004252.
XX PR 14-SEP-2001; 2001US-0318967P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX P1 Bachmann MF, Storni T, Lechner F;
XX DR WO2003-363095/34.
XX PT A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, or immunizing or treating tumors or infectious diseases, e.g. viral infections.
XX PS Disclosure; Page 239-240; 243pp; English.
XX CC The present invention describes a composition (C) for enhancing an immune response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a VLP capable of being recognised by the immune system of the animal. Also described: (1) enhancing an immune response against an antigen or a VLP

CC in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral protection in an animal comprising introducing (C) into the animal. (C) has cytotoxic, virucide, antibacterial, antiparasitic, fungicide, antithyroid, immunosuppressive, antiaddictive, antiinflammatory, antirheumatic and antiarthritic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or treating tumour and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69838 to ACC6952 and ABR56401 to ABR56509 represent sequences used in the exemplification of the present invention.

Sequence 131 AA;

Query Match 100.0%; Score 668; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPITSTANKIVWSPDPTRLSTTFASLIIQRVKVIAELANNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPITSTANKIVWSPDPTRLSTTFASLIIQRVKVIAELANNVSGQYVSVYKRPAP 60
QY 61 KPEGCADACVIMPNENOSRTVTIGSAENLATIKAEWETHKRNDTLFASGNAGLGFIDP 120
Db 61 KPEGCADACVIMPNENOSRTVTIGSAENLATIKAEWETHKRNDTLFASGNAGLGFIDP 120
QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 2
ABU09694 standard; protein; 131 AA.

XX ABU09694;

XX DT 03-JUL-2003 (first entry)

XX DE Bacteriophage AP205 coat protein.

XX KW Bacteriophage AP205; coat protein; hypotensive; cerebroprotective; cardiotonic; nephrotropic; ophthalmological; immunostimulant; vaccine; angiotensin peptide moiety carrier conjugate; angiotensin peptide; renin-activated angiotensin system; hypertension; stroke; infarction; congestive heart failure; kidney failure; retinal haemorrhage.

XX OS Bacteriophage AP205.

XX PN WO2003031466-A2.

XX PD 17-APR-2003.

XX PP 07-OCT-2002; 2002WO-EP011219.

XX PR 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-033105P.

PR 18-JAN-2002; 2002US-0050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396637P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PA (MAURER P.

PI TISSOT A.

DR WPI; 2003-430264/40.
N-PSDB; ABX9523.

XX New angiotensin peptide moiety carrier conjugate comprising a carrier and an angiotensin peptide moiety, useful for treating or preventing a disorder associated with renin-activated angiotensin, e.g. hypertension or infarction.

XX Disclosure: Page 96; 97pp; English.

CC The invention describes an angiotensin peptide moiety carrier conjugate comprising: (a) a carrier with at least one first attachment site; and (b) at least one angiotensin peptide moiety with at least one second attachment site. The angiotensin peptide conjugate and compositions comprising them are useful for immunising an animal against an angiotensin peptide, and for treating or preventing a physical disorder associated with renin-activated angiotensin system such as hypertension, stroke, infarction, congestive heart failure, kidney failure, and retinal haemorrhage. The conjugate is also useful for inducing immune responses, including producing antibodies. This is the amino acid sequence of a bacteriophage AP205 coat protein used in the preparation of the vaccine conjugates of the invention

XX Sequence 131 AA;
SQ Query Match 100.0%; Score 668; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PQ Sequence 131 AA;

Query	Match	Score	Length
QY	1 MANKPMQPITSTANKIVWSPDPTRLSTTFASLIIQRVKVIAELANNVSGQYVSVYKRPAP	60	131
Db	1 MANKPMQPITSTANKIVWSPDPTRLSTTFASLIIQRVKVIAELANNVSGQYVSVYKRPAP	60	131
QY	61 KPEGCADACVIMPNENOSRTVTIGSAENLATIKAEWETHKRNDTLFASGNAGLGFIDP	120	120
Db	61 KPEGCADACVIMPNENOSRTVTIGSAENLATIKAEWETHKRNDTLFASGNAGLGFIDP	120	120
QY	61 KPEGCADACVIMPNENOSRTVTIGSAENLATIKAEWETHKRNDTLFASGNAGLGFIDP	120	120
Db	61 KPEGCADACVIMPNENOSRTVTIGSAENLATIKAEWETHKRNDTLFASGNAGLGFIDP	120	120
QY	121 TAAIVSSDTTA 131	131	131
Db	121 TAAIVSSDTTA 131	131	131

RESULT 3
ABR44611
ID ABR44611 standard; protein; 131 AA.

AC ABR44611;

AC XX DT 25-JUL-2003 (first entry)

DE XX DT 25-JUL-2003 (first entry)

DE AP205 coat protein SEQ ID NO:80.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV; hepatitis B virus; lymphocytic choriomeningitis virus; vaccine; immunostimulant; cytostatic; antiallergic; viricide; antibacterial; immune response; immunisation; allergy; tumour; breast cancer; neuroblastoma; leukaemia; viral disease; influenza; tuberculosis; measles; chicken pox; bacterial infection; synthetic.

XX OS XX WO2003024481-A2.

XX PD 27-MAR-2003.

XX PN XX 16-SEP-2002; 2002WO-1B004132.

PR 14-SEP-2001; 2001US-0318994P.

PR 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PA (MAURER P.

PI TISSOT A.

PA	SCHWARZ K.	KW	first attachment site; antigen; antigenic determinant; prion protein;
PA	(MEIJ)	KW	PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
PA	(LIPO)	KW	prion disease; Bovine Spongiform Encephalopathy; BSE;
PA	(PUMP)	KW	Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
PA	(CIEL)	XX	
PA	(CIELNS)	XX	
PA	(RENH)	OS	Bacteriophage AP205.
XX		PN	WO2003059386-A2.
PI	Tissot A., Schwarz K., Meijerink E., Lipowsky G., Pompens P., Cielens I., Renhofa R., Bachmann MF., Storni T;	XX	XX
PI	XX	PD	24-JUL-2003.
DR	XX	XX	24-JUL-2003; 2003WO-EP000460.
XX	XX	PF	17-JAN-2003;
PT	New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.	PR	18-JAN-2002; 2002US-00050902.
PT	XX	PR	21-JAN-2002; 2002WO-IB000166.
PT	XX	PR	08-JUL-2002; 2002US-0393725P.
PS	Disclosure; Page 319; 322PP; English.	XX	18-JUL-2002; 2002US-0396530P.
XX	XX	PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.
CC	The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance is bound to the VLP. The immunostimulatory substance is useful for enhancing an immune response in an animal by introducing (C) into the animal; (2) Producing (C) for enhancing an immune response in an animal; (3) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; and (4) immunising or treating an animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (c) boosting a T cell response in the animal by administering the vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and antibacterial activities. (C) can be used in vaccines for enhancing an immune response in an animal, particularly a mammal or human.	XX	A vaccine composition for preventing or treating prion diseases (e.g. Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.
CC	Specifically, (C) is useful for enhancing a B cell response, a T cell response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine comprising (C) can also be used for immunising or treating an animal, e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, reptiles or fish. (C) is particularly useful in prophylactic or therapeutic vaccines against allergies, tumours (e.g. breast cancers, neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis, measles or chicken pox), or bacterial infections (e.g. tuberculosis, pneumonia or syphilis). ACG69790 to AC69815 and ABR44502 to ABR4612 represent sequences used in the exemplification of the present invention	XX	This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (PrP) or its dimer, or a PrP peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob disease. The present sequence is that of a RNA-phage AP205 coat protein which is related to the invention.
CC	Sequence 131 AA;	XX	Sequence 131 AA;
CC	Score 668; DB 6; Length 131;	Qy	Query Match 100.0%; Score 668; DB 7; Length 131;
CC	Best Local Similarity 100.0%; Pred. No. 3.9e-73;	Db	Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1 MANKPMQPTSTANKIVWSDPTRLSTSIFASILRQRVKVGLAELNNVSGOTYSYKRPAP 60
Db	1 MANKPMQPTSTANKIVWSDPTRLSTSIFASILRQRVKVGLAELNNVSGOTYSYKRPAP 60	Db	1 MANKPMQPTSTANKIVWSDPTRLSTSIFASILRQRVKVGLAELNNVSGOTYSYKRPAP 60
Qy	61 KPEGCADCVIMPNENQIRTIVSAGSAARNLATKAENETHKRNDTFLFASGNAGLGFLDP 120	Qy	61 KPEGCADCVIMPNENQIRTIVSAGSAARNLATKAENETHKRNDTFLFASGNAGLGFLDP 120
Db	61 KPEGCADCVIMPNENQIRTIVSAGSAARNLATKAENETHKRNDTFLFASGNAGLGFLDP 120	Db	61 KPEGCADCVIMPNENQIRTIVSAGSAARNLATKAENETHKRNDTFLFASGNAGLGFLDP 120
Qy	121 TAAIVSSDTTA 131	Qy	121 TAAIVSSDTTA 131
Db	121 TAAIVSSDTTA 131	Db	121 TAAIVSSDTTA 131
RESULT 4		RESULT 5	
ADD24202	ID ADD24202 standard; protein; 131 AA.	ADD82145	ADJ82145 standard; protein; 131 AA.
XX	XX	XX	XX
AC	AC	AC	AC
XX	XX	XX	XX
DT	15-JAN-2004 (First entry)	DT	06-MAY-2004 (First entry)
XX	Bacteriophage AP205 coat protein #1.	XX	Protein for RANKL antigen array to treat bone disease.
DB		DE	
XX		XX	

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.

XX Unidentified.
OS Unidentified.

PN WO2003039225-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-EPO12449.

XX PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-IB000166.

PR 19-JUL-2002; 2002US-039636P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Bachmann M, Maurer P, Spohn G;

XX DR WPI; 2003-441430/41.

XX PT New compositions comprising a core particle and at least one antigen or antigenic determinant, useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies.

XX Disclosure: SEQ ID NO 112; 222pp; English.

XX The invention relates to a composition comprising a core particle having at least one first attachment site, and at least one antigen or antigenic determinant having at least one second attachment site. The antigen or antigenic determinant is a RANKL protein, RANKL fragment or RANKL peptide. The second attachment site is (non-) naturally occurring with the antigen or antigenic determinant, and is capable of association to the first attachment site. The antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful as a medicament, or for the manufacture of a medicament for treating bone diseases. The composition is especially useful for a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies, and for stimulating mammalian immune system. This sequence represents a protein of the invention.

XX Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPITSTANKIVWDSPTRLSTTFASLLRQVRKGIAELNNVSGQQVSVYKRPA 60

Db 1 MANKPMQPITSTANKIVWDSPTRLSTTFASLLRQVRKGIAELNNVSGQQVSVYKRPA 60

Qy 61 KPEGCAADAVIMPENQSRTVISGSAENLATIKAEWETHKRNVDTLFASGNAGLGFDP 120

Db 61 KPEGCAADAVIMPENQSRTVISGSAENLATIKAEWETHKRNVDTLFASGNAGLGFDP 120

Qy 121 TAAIVSSDDTA 131

Db 121 TAAIVSSDDTA 131

KW interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

OS Unidentified.

PN WO2003040164-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-EPO12445.

XX PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-IB000166.

PR 19-JUL-2002; 2002US-039636P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Bachmann M, Jennings G, Sonderegger I;

XX DR WPI; 2003-441518/41.

XX PT Composition ordered and repetitive antigen or antigenic determinant array, useful as a medicament, or for manufacturing a medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT PT Hodgkin's lymphoma.

XX Disclosure: SEQ ID NO 80; 245pp; English.

XX PS Disclosure; SEQ ID NO 80; 245pp; English.

CC The invention relates to a composition comprising a virus-like particle and at least one antigen, which is a protein or peptide of interleukin (IL-5, IL-13 or eotaxin, and is bound to the virus-like particle, or a core particle with at least one first attachment site and at least one antigen with at least one second attachment site, where the antigen is a protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site is an attachment site naturally or not naturally occurring with the antigen or antigenic determinant. The second attachment site is capable of association to the first attachment site, and where the antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The compositions are useful as medicaments, or for manufacturing a medicament for treating allergic eosinophilic diseases, e.g. asthma, or

CC CC association to form an ordered and repetitive antigen array. The compositions are useful as medicaments, or for manufacturing a medicament or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or

CC CC Hodgkin's lymphoma and related diseases. This sequence is used to generate the compound of the invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;

Best Local Similarity 100.0%; Pred. No. 3.9e-73;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPITSTANKIVWDSPTRLSTTFASLLRQVRKGIAELNNVSGQQVSVYKRPA 60

Db 1 MANKPMQPITSTANKIVWDSPTRLSTTFASLLRQVRKGIAELNNVSGQQVSVYKRPA 60

Qy 61 KPEGCAADAVIMPENQSRTVISGSAENLATIKAEWETHKRNVDTLFASGNAGLGFDP 120

Db 61 KPEGCAADAVIMPENQSRTVISGSAENLATIKAEWETHKRNVDTLFASGNAGLGFDP 120

Qy 121 TAAIVSSDDTA 131

Db 121 TAAIVSSDDTA 131

XX anti-allergic; cytosatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage AP205;
 KW coat protein; VLP; adjuvant.
 XX Bacteriophage AP205.
 XX WO2004000351-A1.
 XX PD 31-DEC-2003.
 XX PR 20-JUN-2003; 2003MO-EP006541.
 XX PR 20-JUN-2002; 2002US-0389898P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX P1 Bachman MF, Renner WA;
 XX DR WPI; 2004-108361/11.
 XX PS Example 16; SEQ ID NO 90; 252pp; English.
 PT New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with
 PT the VLP, useful for enhancing immune response or for treating e.g. tumors
 PT or chronic viral diseases.
 XX Example 17; SEQ ID NO 91; 252pp; English.
 CC The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage AP205
 CC coat protein a virus like particle (VLP) that can be used in the adjuvant
 CC of the invention.
 XX Sequence 131 AA:
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Sequence 131 AA:
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKPMQPTSTANKIVWSDPTRLSTPSASLIRQRVKVIAFLNNVSGQTVSYKRPAP 60
 Db 1 MANKPMQPTSTANKIVWSDPTRLSTPSASLIRQRVKVIAFLNNVSGQTVSYKRPAP 60
 Qy 61 KPGGCADACVIMNENQSIIRTIVSGSAENLATKAENETHKRNVDTLFASGNAGLGLDP 120
 Db 61 KPGGCADACVIMNENQSIIRTIVSGSAENLATKAENETHKRNVDTLFASGNAGLGLDP 120
 Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131
 Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131

RESULT 8
 ADI40710
 ID ADI40710 standard; protein; 131 AA.
 XX AC ADI40710;
 XX DT 22-APR-2004 (first entry)
 XX DE Bacteriophage AP205 coat protein SEQ ID NO:1.
 XX OS Bacteriophage AP205.

XX PN WO2004007538-A2.
 XX PD 22-JAN-2004.
 XX PR 14-JUL-2003; 2003WO-EP007572.
 XX PR 17-JUL-2002; 2002US-0396126P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX P1 Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;
 XX DR WPI; 2004-122882/12.
 XX N-PSTDDB; ADI0711.
 XX PT New virus-like particle, useful for preparing a composition for treating
 PT or preventing a disease e.g., cancer, allergy or asthma.
 XX Claim 1; SEQ ID NO 1; 170pp; English.
 XX CC The present invention describes a virus-like particle (1) which
 CC comprises: (a) a protein having the 131-amino acid sequence of
 CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
 CC or ADI0712 respectively; or
 CC (b) a mutant of the protein of (a). Also
 CC described: (1) a recombinant protein having the 131-amino
 CC acid sequence; (2) a vector for producing a AP205 virus like particle
 CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
 CC identical to that of the sequence comprising 3635 or 3613 bp or producing
 CC a recombinant protein comprising a nucleotide sequence encoding a
 CC polypeptide fused to a protein; (3) a pharmaceutical composition
 CC comprising the composition and a carrier; (4) a process for producing a
 CC non-naturally occurring, ordered and repetitive antigen array; (5) a
 CC method of treating or preventing a disease, disorder or physiologic
 CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
 CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
 CC (8) a method of producing the virus-like particle. (1) has cytostatic
 CC activity, and can be used in vaccines, and in gene therapy. The virus-
 CC like particle is useful for preparing a composition for treating or
 CC preventing a disease e.g., cancer, allergy or asthma. The present
 CC sequence represents the bacteriophage AP205 coat protein, which is used
 CC in the exemplification of the present invention.

XX SQ Sequence 131 AA:
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKPMQPTSTANKIVWSDPTRLSTPSASLIRQRVKVIAFLNNVSGQTVSYKRPAP 60
 Db 1 MANKPMQPTSTANKIVWSDPTRLSTPSASLIRQRVKVIAFLNNVSGQTVSYKRPAP 60
 Qy 61 KPGGCADACVIMNENQSIIRTIVSGSAENLATKAENETHKRNVDTLFASGNAGLGLDP 120
 Db 61 KPGGCADACVIMNENQSIIRTIVSGSAENLATKAENETHKRNVDTLFASGNAGLGLDP 120
 Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131
 Qy 121 TAAIVSSDTA 131
 Db 121 TAAIVSSDTA 131

RESULT 9
 ADJ67170
 ID ADJ67170 standard; protein; 131 AA.
 XX AC ADJ67170;
 XX DT 06-MAY-2004 (first entry)
 XX DE Bacteriophage AP205 coat protein for antigen display array.
 XX KW virus-like particle; bacteriophage AP205; coat protein; cytostatic;
 KW vaccine; gene therapy; cancer; allergy; asthma.
 XX OS Bacteriophage AP205.

KW antigenic array.
 XX Bacteriophage AP205.
 OS WO2004016282-A1.
 XX PN
 XX PD 26-FEB-2004.
 XX PR 18-JUL-2003; 2003WO-EP007864.
 XX PP 19-JUL-2002; 2002US-0396639P.
 XX PR 15-MAY-2003; 2003US-0470432P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 XX PI Bachmann MF, Tissot A, Ortmann R, Lueoend R, Staufenbiel M;
 PI Frey P;
 DR XX WPI; 2004-203731/19.
 PT Composition comprising a core particle with at least one attachment site,
 PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 PT such as Alzheimer's disease.
 XX PS Claim 12; SEQ ID NO 28; 184PP; English.
 XX PS Claim 12; SEQ ID NO 28; 184PP; English.
 CC The invention relates to a new composition comprising: (i) a core particle
 CC with at least one first attachment site; and (ii), at least one
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is Ghrelin or Ghrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the Ghrelin or a
 CC Ghrelin Peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC AP205 coat protein which can used as part of the repetitive or antigenic
 CC array.
 XX Sequence 131 AA:
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKEMQPTSTANKIVWDSDPTRLSTTFASILLRQRVKGIAELNNVSCQQVSYKRKAP 60
 Db 1 MANKEMQPTSTANKIVWDSDPTRLSTTFASILLRQRVKGIAELNNVSCQQVSYKRKAP 60
 Qy 61 KPEGGADAVCIMPNENOSIRTVISGSAENLATIKAEWETHKRNYDTLFPASGNAGLGFIDP 120
 Db 61 KPEGGADAVCIMPNENOSIRTVISGSAENLATIKAEWETHKRNYDTLFPASGNAGLGFIDP 120
 Qy 121 TAATVSSDDTA 131
 Db 121 TAATVSSDDTA 131
 SQ Sequence 131 AA:
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKEMQPTSTANKIVWDSDPTRLSTTFASILLRQRVKGIAELNNVSCQQVSYKRKAP 60
 Db 1 MANKEMQPTSTANKIVWDSDPTRLSTTFASILLRQRVKGIAELNNVSCQQVSYKRKAP 60
 Qy 61 KPEGGADAVCIMPNENOSIRTVISGSAENLATIKAEWETHKRNYDTLFPASGNAGLGFIDP 120
 Db 61 KPEGGADAVCIMPNENOSIRTVISGSAENLATIKAEWETHKRNYDTLFPASGNAGLGFIDP 120
 Qy 121 TAATVSSDDTA 131
 Db 121 TAATVSSDDTA 131
 SQ Sequence 131 AA:
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKEMQPTSTANKIVWDSDPTRLSTTFASILLRQRVKGIAELNNVSCQQVSYKRKAP 60
 Db 1 MANKEMQPTSTANKIVWDSDPTRLSTTFASILLRQRVKGIAELNNVSCQQVSYKRKAP 60
 Qy 61 KPEGGADAVCIMPNENOSIRTVISGSAENLATIKAEWETHKRNYDTLFPASGNAGLGFIDP 120
 Db 61 KPEGGADAVCIMPNENOSIRTVISGSAENLATIKAEWETHKRNYDTLFPASGNAGLGFIDP 120
 Qy 121 TAATVSSDDTA 131
 Db 121 TAATVSSDDTA 131
 RESULT 10
 ADKS2204 ID ADKS2204 standard; protein; 131 AA.
 AC ADKS2204;
 XX DT 20-MAY-2004 (first entry)
 DE Bacteriophage AP205 coat protein.
 XX DE Bacteriophage AP205 coat protein.
 KW neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
 KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
 KW drug addiction; fentanyl; heroin; morphine; amphetamine; cocaine;

KW	methyleneoxymethamphetamine; methamphetamine; methylphenidate;	KW	cystostatic; virucide; antibacterial; antiparasitic; fungicide;
KW	nicotine; cotinine; nornicotine; PCP; LSD; mescaline; psilocybin;	KW	antiallergic; immunosuppressive; antiaddictive; antinflammatory;
KW	tetrahydrocannabinol; diazepam; desipramine; imipramine; nortriptyline;	KW	antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
KW	amitriptyline; coat protein.	KW	anti-rheumatic; antiarthritic; vaccine; immunisation; infectious disease;
XX	Bacteriophage AP205.	XX	anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
OS	W02004009116-A2.	XX	graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
XX		XX	Alzheimer's disease; osteoporosis; rheumatoid arthritis; multiple sclerosis;
PN		XX	inflammatory autoimmune disease.
XX		OS	
PD	29-JAN-2004.	XX	Synthetic.
XX	18-JUL-2003; 2003WO-EP007859.	XX	WO2003024480-A2.
PF	18-JUL-2002; 2002US-0396575P.	XX	27-MAR-2003.
PR		XX	16-SEP-2002; 2002WO-IB004222.
XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.	XX	14-SEP-2001; 2001US-0318967P.
PA		XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.
XX		XX	PI Bachmann MF, Storni T, Lechner F;
PA		XX	WPI, 2003-363095/34.
XX		XX	A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, or immunizing or treating tumors or infectious diseases, e.g. viral infections.
PS		XX	Disclosure; Page 240-241; 243PP; English.
XX		XX	The present invention describes a composition (C) for enhancing an immune response against an antigen or a virus-like particle (VLP) bound to at least one antigen, or a VLP capable of being recognised by the immune system of the animal. Also described: (1) enhancing an immune response against an antigen or a VLP in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral protection in an animal comprising introducing (C) into the animal. (C) has cyrostatic, virucide, antibacterial, antiparasitic, fungicide, antiallergic, immunosuppressive, antiaddictive, antiinflammatory, antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic, anti-rheumatic and antiarthritic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69838 to ACR6852 and ABR56401 to ABR5509 represent sequences used in the exemplification of the present invention
XX		XX	Sequence 131 AA;
PS	SEQ ID NO 14; 141PP; English.	XX	Score 668; DB 8; Length 131;
CC	The invention comprises a hapten-carrier conjugate consisting of a carrier (e.g. a recombinant virus protein) that has at least one attachment site, and at least one hapten with at least one second attachment site. The method of the invention is useful for treating or	CC	Best Local Similarity 100.0%; Pred. No. 3.9e-73; Indels 0; Gaps 0;
CC	morphine, addiction to a drug, such as: codeine, fentanyl, heroin, morphine, amphetamine, cocaine, methamphetamine, nicotine, nornicotine, PCP, methamphetamine, methylphenidate, nicotine, cotinine, tetrahydronannabinol, diazepam, desipramine, LSD, mescaline, psilocybin, tetrahydronannabinol, diazepam, desipramine, imipramine, nortriptyline and the amitriptyline class of drugs. The method of the invention is also useful for preventing and treating diseases associated with addiction. The present amino acid sequence represents a protein which is claimed for use in the hapten-carrier conjugate of the invention.	CC	Matches 131; Conservative 0; Mismatches 0; Gaps 0;
CC	Sequence 131 AA;	CC	Query Match 100.0%; Score 660; DB 6; Length 131;
CC	Qy 1 MANKPMQPTSTANKIVASDPTRLSTTSFASLIRQVRKGIAELNNVSGQQYISVYKRPAP 60	CC	Best Local Similarity 99.2%; Pred. No. 3.7e-72; Matches 130; Conservative 0; Mismatches 1; Gaps 0;
Db	1 MANKPMQPTSTANKIVASDPTRLSTTSFASLIRQVRKGIAELNNVSGQQYISVYKRPAP 60	CC	Query 1 MANKPMQPTSTANKIVASDPTRLSTTSFASLIRQVRKGIAELNNVSGQQYISVYKRPAP 60
Qy	61 KPGECADAVIMENENQSRTVSGAENLATKAENETHKRNVDTLFASGNAGLGFDP 120	CC	DB 1 MANKPMQPTSTANKIVASDPTRLSTTSFASLIRQVRKGIAELNNVSGQQYISVYKRPAP 60
Db	61 KPGECADAVIMENENQSRTVSGAENLATKAENETHKRNVDTLFASGNAGLGFDP 120	CC	Qy 61 KPGECADAVIMENENQSRTVSGAENLATKAENETHKRNVDTLFASGNAGLGFDP 120
Qy	61 KPGECADAVIMENENQSRTVSGAENLATKAENETHKRNVDTLFASGNAGLGFDP 120	CC	DB 61 KPGECADAVIMENENQSRTVSGAENLATKAENETHKRNVDTLFASGNAGLGFDP 120
Db	121 TAAIVSSDDTA 131	CC	Qy 121 TAAIVSSDDTA 131
Db	121 TAAIVSSDDTA 131	CC	DB 121 TAAIVSSDDTA 131
RESULT 12			
ID	ABR56509 standard; protein: 131 AA.		
XX			
AC	ABR56509;		
XX			
DT	28-JUL-2003 (First entry)		
XX			
DE	AP205 coat protein SEQ ID NO:81.		
XX			
RW	Antigen presenting cell; APC; immune response; virus like particle; VLP;		

Db	121 TAAIVSSDTTA 131	Db	1 MANKPMQPTTSTANKIVWSDPTRLSTTSASLIRQRVKVIAELNNVSGQQYVSYKRPAP 60
RESULT 13			
ID	ABU09695	Qy	61 KPESCADACVIMPNENQSIIRTIVSGAENLATIKAENETHKRNDTUFASGNAGLFDP 120
ID	ABU09695 standard; protein; 131 AA.	Db	61 KPESCADACVIMPNENQSIIRTIVSGAENLATIKAENETHKRNDTUFASGNAGLFDP 120
XX		Qy	121 TAAIVSSDTTA 131
AC	ABU09695;	Db	121 TAAIVSSDTTA 131
XX		DT	03-JUL-2003 (first entry)
DE	Bacteriophage AP205 coat protein mutant.	RESULT 14	
XX	Bacteriophage AP205; coat protein; hypotensive; cerebroprotective; cardiotonic; nephrotropic; ophthalmological; immunostimulant - vaccine; angiotensin Peptide moiety carrier conjugate; angiotensin peptide; renin-activated angiotensin system; hypertension; stroke; infarction; congestive heart failure; kidney failure; retinal haemorrhage; mutant; murein.	ABR44612	ABR44612 standard; protein; 131 AA.
OS		ID	ABR44612
XX		XX	KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine; immunostimulant; cytotoxic; antiallergic; viricide; antibacterial; immune response; immunisation; allergy; tumour; breast cancer; neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles; chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
PD	Bacteriophage AP205.	XX	KW
PD		DE	AP205 coat protein SEQ ID NO:81.
PP		XX	Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
PP	Location/Qualifiers 5	KW	hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
FT	/note= "Wild type Pro substituted by Thr"	KW	immunostimulant; cytotoxic; antiallergic; viricide; antibacterial;
NN	WO2003031466-A2.	KW	immune response; immunisation; allergy; tumour; breast cancer;
PN		KW	neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles; chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
PD	17-APR-2003.	XX	KW
PP	07-OCT-2002; 2002WO-EP011219.	OS	Synthetic.
PP		XX	
XX		PN	WO2003024481-A2.
PR	05-OCT-2001; 2001US-0326998P.	XX	
PR	07-NOV-2001; 2001US-0331045P.	PD	27-MAR-2003.
PR	18-JAN-2002; 2002US-0050902.	XX	
PR	21-JAN-2002; 2002WO-1B000166.	PF	16-SEP-2002; 2002WO-1B004132.
PR	19-JUL-2002; 2002US-0396637P.	XX	
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	PR	14-SEP-2001; 2001US-0318994P.
XX		PR	22-APR-2002; 2002US-0374145P.
XX		XX	
PA	Bachmann M;	(CYTO-)	CYTOS BIOTECHNOLOGY AG.
XX		PA	MAURER P.
DR	WPI: 2003-430264/40.	PA	(MAUR/)
DR	N-PSDB; ABX95524.	PA	TISSOT A.
XX		PA	(TISS/)
XX		PA	SCHWARZ K.
XX		PA	(SCHW/)
XX		PA	MELCIERINK E.
XX		PA	(MEIJ/)
XX		PA	LIPOWSKY G.
PT	New angiotensin peptide moiety carrier conjugate comprising a carrier and an angiotensin peptide moiety, useful for treating or preventing a disorder associated with renin-activated angiotensin, e.g. hypertension or infarction.	PA	(PUMP/)
PT		PA	PUMPENS P.
PT		PA	(CIEL/)
PT		PA	CIELENS I.
PT		PA	(RENH/)
PA		PA	RENHORA R.
XX		XX	
PI	Bachmann M;	PI	Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
XX		PI	Cieleens I, Renhora R, Bachmann MF, Storni T;
DR		XX	
DR	WPI: 2003-354564/33.	XX	
CC The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance. The immunostimulatory substance is packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.			
CC Disclosure; Page 319-320; 322pp; English.			
CC The invention describes an angiotensin peptide moiety carrier conjugate comprising: (a) a carrier with at least one first attachment site; and (b) at least one angiotensin peptide moiety with at least one second attachment site. The angiotensin peptide conjugate and compositions comprising them are useful for immunising an animal against an angiotensin peptide, and for treating or preventing a physical disorder associated with renin-activated angiotensin system such as hypertension, stroke, infarction, congestive heart failure, kidney failure, and retinal haemorrhage. The conjugate is also useful for inducing immune responses, including producing antibodies. This is the amino acid sequence of a bacteriophage AP205 coat protein mutant based on the wild type sequence shown in ABU09694 and used in the preparation of the vaccine conjugates of the invention.			
CC Sequence 131 AA;			
CC Query Match 98.8%; Score 660; DB 6; Length 131;			
CC Best Local Similarity 99.2%; Pred. No. 3 7e-72;			
CC Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
CC (C) boosting a T cell response in the animal by administering the vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and			
CC Query			

CC antibacterial activities. (I) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC comprising (C) or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC6915 to AC6915 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 131 AA;

Query Match 98.8%; Score 660; DB 6; Length 131;

Best Local Similarity 99.2%; Pred. No. 3.7e-72; Matches 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MANKPMQPTSTANKIVWSDPTRLSTPSASLIRQRYKVGIAELNNVSGQYVSYKRPA	60
Db	1	MANKTMQPTSTANKIVWSDPTRLSTPSASLIRQRYKVGIAELNNVSGQYVSYKRPA	60
Qy	61	KPGEGCADCVIMPNENOSIRTIVSGSAEMLATKAEMETHKRNVDTLFASGNAGLGFLDP	120
Db	61	KPGEGCADCVIMPNENOSIRTIVSGSAEMLATKAEMETHKRNVDTLFASGNAGLGFLDP	120
Qy	121	TAIIIVSSDTTA 131	
Db	121	TAIIIVSSDTTA 131	

RESULT 15

ID ADD24203 standard; protein; 131 AA.

XX AC

XX DT 15-JAN-2004 (first entry)

XX DE Bacteriophage AP205 coat protein #2.
 XX vaccine composition; virus-like particle; core particle;
 XX first attachment site; antigen; antigenic determinant; prion protein;
 XX PrP; PrP peptide; peptide; vaccine; neuroprotective; antiinflammatory;
 XX prion disease; Bovine Spongiform Encephalopathy; BSE;
 XX Creutzfeldt-Jakob Disease; prion; AP205; coat protein.

XX Synthetic.

XX Bacteriophage AP205.

XX PN WO2003059386-A2.

XX PD 24-JUL-2003.

XX PP 17-JAN-2003; 2003WO-EP000460.

XX PR 18-JAN-2002; 2002US-00050902.

XX PR 21-JAN-2002; 2002WO-18900166.

XX PR 08-JUL-2002; 2002US-039725B.

XX PR 18-JUL-2002; 2002US-0396590P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Pellicoli E, Renner WA,

XX DR WPI; 2003-598483/56.

XX DR N-PSDB; ADD24204.

XX PR A vaccine composition for preventing or treating prion diseases (e.g.

PR Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

CC Disclosure; SEQ ID NO 96; 246pp; English.
 CC This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC or treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC disease. The present sequence is that of a mutant RNA-phage AP205 coat
 CC protein which is related to the invention.

XX SQ Sequence 131 AA;

Query Match	Score	DB	Length
Best Local Similarity	98.8%	660	131;
Matches	99.2%	7	131;
Conservative	99.2%	72	72;
Mismatches	0	No. 3.7e-72;	
Indels	0	Pred. No. 3.7e-72;	
Gaps	0	Matches 130; Conservative	
Score	98.8%	Score 660;	
Length	131;	DB 7;	
XX	XX	XX	
Qy	1	MANKPMQPTSTANKIVWSDPTRLSTPSASLIRQRYKVGIAELNNVSGQYVSYKRPA	60
Db	1	MANKTMQPTSTANKIVWSDPTRLSTPSASLIRQRYKVGIAELNNVSGQYVSYKRPA	60
Qy	61	KPGEGCADCVIMPNENOSIRTIVSGSAEMLATKAEMETHKRNVDTLFASGNAGLGFLDP	120
Db	61	KPGEGCADCVIMPNENOSIRTIVSGSAEMLATKAEMETHKRNVDTLFASGNAGLGFLDP	120
Qy	121	TAIIIVSSDTTA 131	
Db	121	TAIIIVSSDTTA 131	
Qy	121	TAIIIVSSDTTA 131	
Db	121	TAIIIVSSDTTA 131	

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